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8E15

Please search **SEQ ID NOS.: 3, 4, 7, 8, and 9** from the aforementioned application (09/877,606) v. all relevant databases, including interference.

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Toby Port
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PT Production of constrained helical peptide(s) by linking side chains
PT on termini of octa-peptide - derived from human immunodeficiency
PT virus gp41 protein, useful in vaccines for treatment and prevention
PT of infection

PS Claim 11; Page 156; 279pp; English.

CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins
CC of known HIV virus strains (AAY22871, AAY22880, AAY22888 and
CC AAY22903 represent consensus sequences of various sections of the gp41
CC protein). Sequences derived from the peptides are used to produce
CC constrained helical peptides of the invention. The constrained helical
CC peptide is produced by synthesizing an octapeptide in which both terminal
CC amino acids have a side-chain that includes a group able to form an amide
CC bond, and cyclizing the octapeptide by reacting the specified side-chain
CC residues with a difunctional linker to produce two amide bonds.
CC The constrained helical peptides are used to treat or prevent HIV
CC infection, especially as vaccines that generate antibodies that
CC prevent viral membrane fusion or infectivity. Vaccines may contain
CC constrained helical peptides derived from several different strains of
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other
CC uses for the constrained helical peptides are in affinity purification
CC of ligands (particularly where complete binding protein is not readily
CC available, e.g. replacements for protein A in immunoglobulin
CC purification); as epitope mimics for antibody production; for isolation
CC of synthetic antibody clones from phage display libraries; or as stable
CC forms of "floppy" peptides or proteins.

CC Sequence 268 AA;

Query Match 99.3%; Score 290; DB 19; Length 268;
Best Local Similarity 98.1%; Pred. No. 1.6e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLIHSLESQNOQEKNEQELLDKRWASIMWFI 52
DB 154 NHTTWLEMDREINNTYSLIHSLESQNOQEKNEQELLDKRWASIMWFI 205

RESULT 2
ABG68291
ID ABG68291 standard; Protein; 268 AA.

AC ABG68291;

DT 07-OCT-2002 (first entry)

DE Envelope protein gp41 from HIV clade B strain #10.

KM HIV, glycoprotein; gp41; antigen; helical conformation;
KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
KM viral envelope protein; vaccine; virucide; anti-HIV.

OS Human immunodeficiency virus type 1 clade B.

OS US6271198-B1.

PD 07-AUG-2001.

PF 05-NOV-1997; 97US-0965056.

PR 16-JUN-1997; 97US-049787P.

PR 06-NOV-1996; 96US-0743699.

PR 16-JUN-1997; 97US-0876698.

PA (GENET) GENENTECH INC.

PI Brasted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
PI WPI; 2002-487624/52.

PT New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have
PT alpha-helical conformation

PS Disclosure; Column 151-154; 175pp; English.

CC The invention relates to cyclic peptides (A) with a constrained helical
CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
CC protein) of human immunodeficiency virus (HIV). The cyclic
CC peptides have formulas given in the specification part of which are
CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
CC C, D, E or O. The peptides are used to cause induction of a specific
CC immune response, resulting in antibodies that prevent virus-induced
CC membrane fusion. The peptides are used to treat subjects with, or
CC of, HIV infection, either as antifusion/anti-infection agents or,
CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is gp41 protein from a particular
CC HIV clade used to derive a consensus sequence of gp41.

CC Sequence 268 AA;

Query Match 99.3%; Score 290; DB 23; Length 268;
Best Local Similarity 98.1%; Pred. No. 1.6e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLIHSLESQNOQEKNEQELLDKRWASIMWFI 52
DB 154 NHTTWLEMDREINNTYSLIHSLESQNOQEKNEQELLDKRWASIMWFI 205

RESULT 3
ABB83400
ID ABB83400 standard; protein; 344 AA.

AC ABB83400;

DT 19-SEP-2002 (first entry)

DE HIV gp41 LAI protein #1.

KM HIV, gp41; LAI; virucide; anti-HIV; vaccine; HIV infection.

OS Human immunodeficiency virus.

OS Key Location/Qualifiers

FT Peptide 1..23

FT /label- Fusion_peptide 173..194

FT Domain /label- Transmembrane_domain

FT WO200253587-A2.

PD 11-JUL-2002.

PF 04-JAN-2002; 2002WO-FR00031.

PR 05-JAN-2001; 2001FR-0000141.

PR 23-JAN-2001; 2001FR-0000848.

PA (AVET) AVENTIS PASTEUR.

PI Brasseur R, Charlotiaux B, Chevalier M, El Habib R, Krell T;
PI Sodoyer R;
PI WPI; 2002-528852/56.

PT New mutant human immune deficiency virus gp41 polypeptide, useful in

PT vaccines against human immune deficiency virus, mimics the intermediate
PT state of the native polypeptide
XX
PS Disclosure; Page 29; 29pp; French.
XX
CC The present invention relates to novel mutant HIV gp41 LAI proteins
CC (AB83411-AB83420). The mutants can form a structure corresponding to,
CC or mimicking, the intermediate state of gp41. The mutants, or their
CC conjugate with a carrier, or vectors containing nucleic acid that encode
CC them, are used in vaccines for treatment or prevention of infection by
CC HIV. The present sequence is wild-type HIV gp41 LAI protein, which
CC was used to generate the mutants of the invention.
XX
SQ Sequence 344 AA;
Query Match 99.3%; Score 290; DB 23; Length 344;
Best Local Similarity 98.1%; Pred. No. 2.2e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSLMMNFNI 52
DB 113 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSLMMNFNI 164
RESULT 4
AAR53785
ID AAR53785 standard; Protein; 420 AA.
XX
AC AAR53785;
XX
DT 28-DEC-1994 (first entry)
XX
DE Translation of HIV-1 in the region encoding the gp41 polypeptide.
XX
KM Human immunodeficiency virus; HIV-1; AIDS; lentivirus; TM protein;
KM extracellular protein; transmembrane protein; gp41.
XX
OS HIV-1.
XX
FH Key Location/Qualifiers
FT Protein 43..387
FT /label= gp41
XX
PM WO9412533-A.
XX
PD 09-JUN-1994.
XX
PF 12-JAN-1993; 93WO-US00212.
XX
PR 23-NOV-1992; 92US-0979975.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Essex ME, Lee TH, Yu X;
XX
DR WPI: 1994-200197/24.
DR N-PSDB; AA066275.
XX
PT Method for treating HIV patients - comprises administration of
PT mutated gp41 polypeptide
XX
PS Claim 11; Fig 1; 54pp; English.
XX
CC The inventors claim a method of treating a patient infected with HIV
CC by administering a mutated gp41 polypeptide or a therapeutic
CC composition comprising nucleic acid encoding the mutant gp41
CC polypeptide in an expressible genetic construction. The mutant gp41
CC polypeptide contains a deletion of at least one AA in at least one
CC of the following regions of wild type gp41 (AAR53783): AAs 844-856;
CC 814-856; 796-856; 776-856; 753-856; or 710-856, effective to either
CC disrupt viral replication or HIV or disrupt the assembly of viral
CC Env proteins in an HIV infected cell. AA066275 corresponds to bps 7631-
CC 8890 of wt HIV-1. X in the AA sequence represents the posn. of a

CC stop codon in AA066275.
XX
SQ Sequence 420 AA;
Query Match 99.3%; Score 290; DB 15; Length 420;
Best Local Similarity 98.1%; Pred. No. 2.7e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSLMMNFNI 52
DB 155 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSLMMNFNI 206
RESULT 5
AAM00181
ID AAM00181 standard; Protein; 519 AA.
XX
AC AAM00181;
XX
DT 12-NOV-1996 (first entry)
XX
DE HIV-1 env protein.
XX
KM Poliovirus; encapsidation; capsid; vaccine; genetic immunisation;
KM HIV-1; human immunodeficiency virus type 1; env protein.
XX
OS Human immunodeficiency virus type 1.
XX
PM WO9625173-A1.
XX
PD 22-AUG-1996.
XX
PF 13-FEB-1996; 96WO-US01895.
XX
PR 15-FEB-1995; 95US-0389459.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Ansardl DC, Morrow CD, Porter DC;
XX
DR WPI: 1996-393136/39.
DR N-PSDB; AAT33295.
XX
PT Encapsidation of recombinant polio:virus nucleic acid for use in
PT vaccines - using a polio:virus nucleic acid which lacks the PI
PT capsid region and an expression system which provides the region
XX
PS Disclosure; Page 61-63; 108pp; English.
XX
CC cDNA sequences (AAT33293-95) respectively code for the gag, pol and
CC env proteins (AAM00179-81) of HIV-1. They can be used to substitute
CC the PI capsid gene of poliovirus in recombinant poliovirus nucleic
CC acids (rPNAs). Such rPNAs are encapsidated by introduction into
CC a host cell together with a vaccinia virus or plasmid vector
CC encoding the poliovirus PI capsid precursor protein. Encapsidated
CC rPNAs are useful for genetic immunisation, stimulating an immune
CC response to the HIV-1 protein.
XX
SQ Sequence 519 AA;
Query Match 99.3%; Score 290; DB 17; Length 519;
Best Local Similarity 98.1%; Pred. No. 3.5e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSLMMNFNI 52
DB 420 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSLMMNFNI 471
RESULT 6
AAR69997
ID AAR69997 standard; Protein; 521 AA.
XX

AC AAR69997;
XX
DT 13-SEP-1995 (first entry)
XX
DE HIV-1 env protein.
XX
KM Encapsulation; Human immunodeficiency virus; type 1; immunogenic;
KM poliovirus.
XX
OS Human immunodeficiency virus type 1.
XX
PN CA2125344-A.
XX
PD 02-JAN-1995.
XX
PF 07-JUN-1994; 94CA-2125344.
XX
PR 01-JUL-1993; 93US-0087009.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Morrow CD;
XX
DR WPI: 1995-099021/14.
DR N-PSDB; AAO80575.
XX
PT Method for encapsulating recombinant polio:virus nucleic acid
PT useful for providing comps. to stimulate immune response.
XX
PS Disclosure; Page 38; 62pp; English.
XX
CC The sequence is that of the HIV-1 env protein. The DNA encoding
CC such protein is used in a method (claimed) to encapsulate
CC poliovirus cDNA to make it more immunogenic.
CC See also AAR6995-6.
XX
SQ Sequence 521 AA;
OY Query Match 99.3%; Score 290; DB 16; Length 521;
Best Local Similarity 98.1%; Pred. No. 3.5e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 NHTTLEMDREINNTSLHSIESONQOEKNEDELLEDKRSLWMMENI 52
420 NHTTLEMDREINNTSLHSIESONQOEKNEDELLEDKRSLWMMENI 471
RESULT 7
AAM43066
ID AAM43066 standard; peptide: 853 AA.
XX
AC AAM43066;
XX
DT 11-SEP-1998 (first entry)
XX
DE HIV-1 gp120 protein fragment from isolate HXB2.
XX
KW gp120 protein; purification; fractionation; ion exchange; chromatography;
KW binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN US5696238-A.
XX
PD 09-DEC-1997.
XX
PF 11-MAY-1995; 95US-0439286.
XX
PR 20-AUG-1991; 91US-0684963.
PR 16-AUG-1993; 93US-0109002.
PR 09-MAY-1994; 94US-0240073.
PR 11-MAY-1995; 95US-0439286.
XX

PA (CHIR) CHIRON CORP.
XX
PI Halgwood NL, Scandella C;
XX
DR WPI: 1998-041353/04.
XX
PT Purification of HIV gp120 - using chromatographic methods
XX
PS Disclosure; Fig 2A-W; 53pp; English.
XX
CC AAM43066-W43080 are fragments of the gp120 protein from different human
CC immunodeficiency virus type 1 (HIV-1) isolates. These proteins are used
CC in a novel method for purifying HIV gp120 so as to provide a purified
CC gp120 glycoprotein having protein/protein binding properties
CC substantially identical to natural viral HIV gp120. The method involves
CC glycosylating a crude gp120 preparation containing full-length,
CC glycosylated gp120 using ion exchange chromatography so as to provide a
CC first collection of fractions. A fraction from the first collection is
CC selected that exhibits specific binding affinity for CD4 peptide,
CC thereby producing a first fractionated material. The first fractionated
CC material is fractionated by hydrophobic interaction chromatography so as
CC to provide a second collection of fractions from which a second
CC peptide. This second fraction is fractionated by size exclusion
CC chromatography so as to provide a third collection of fractions
CC exhibiting specific binding affinity for CD4 peptide, thereby providing
CC the purified gp120. The purified gp120 can be used for antibody
CC production and in vaccines.
XX
SQ Sequence 853 AA;
OY Query Match 99.3%; Score 290; DB 19; Length 853;
Best Local Similarity 98.1%; Pred. No. 6.1e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Db 1 NHTTLEMDREINNTSLHSIESONQOEKNEDELLEDKRSLWMMENI 52
621 NHTTLEMDREINNTSLHSIESONQOEKNEDELLEDKRSLWMMENI 672
RESULT 8
AAP60131
ID AAP60131 standard; Protein: 856 AA.
XX
AC AAP60131;
XX
DT 26-JUN-1991 (first entry)
XX
DE Sequence of the AIDS envelope protein.
XX
KW AIDS; HIV; LAV; HTLV-III; vaccine; antibody; epitope; antigen;
KW diagnosis.
XX
OS HTLV-III.
XX
PN EP199301-A.
XX
PD 29-OCT-1986.
XX
PF 18-APR-1986; 86EP-0105371.
XX
PR 19-APR-1985; 85US-0725021.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (USGO) US GOVERNMENT.
PA (HEAL-) DEPT. HEALTH & HUMAN SERV.
PA (USDH) US DEPT HEALTH & HUMAN.
XX
PI Crowl RM, Gallo RC, Reddy EP, Shaw GM, Wong-Staal FY;
XX
DR WPI: 1986-286067/44.
DR N-PSDB; AAP60128.
XX

PT Envelope protein of acquired immune deficiency syndrome virus -
PT useful for improved testing of human blood for antibodies against
PT virus and as antigen for vaccines
XX
XX
PS Claim 33; Fig 6A; 46pp; English.
XX
CC An expression vector contg. a gene (AAN60128) coding for an envelope
CC protein of an AIDS virus, and the envelope protein of an AIDS virus
CC (AAB60131) are claimed. The vector is pref. a member of the pEV/env
CC family, e.g. pEV1.2 or 3/env 44-640 or 205-640.
XX
XX
SQ Sequence 856 AA:

Query Match 99.3%; Score 290; DB 7; Length 856;
Best Local Similarity 98.1%; Pred. No. 6.1e-23;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTWTMEMREINNTSLHSLEESONOEKNEDELELDKASLMNPN 52
DB 624 NHTTMMEMREINNTSLHSLEESONOEKNEDELELDKASLMNPN 675

RESULT 9
AAR41025
ID AAR41025 standard; protein; 856 AA.
XX
AC AAR41025;
XX
DT 23-MAR-1994 (first entry)
XX
DE Selectively deglycosylated HIV-1 HXB2 env gp160 mutain C4.
XX
XX N-linked deglycosylation; gp120; human immunodeficiency virus; type 1;
KW envelope glycoprotein; vaccine; site-directed mutagenesis.
XX
OS Human immunodeficiency virus type 1 (HXB2 strain).
XX
FH
FH Key Location/Qualifiers
FT Peptide 1..30
FT Protein /label= signal_peptide
FT /label= gp120
FT /note= "exterior membrane glycoprotein"
FT Protein 512..856
FT /label= gp41
FT /note= "transmembrane glycoprotein"
FT Modified-site 88
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 136
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 141
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 156
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 160
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 186
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 197
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 230
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 234
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XX

FT Modified-site 241
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 262
FT /label= N-linked_glycosylation_site
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FT Modified-site 276
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FT Modified-site 295
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FT Modified-site 332
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FT Modified-site 356
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FT Modified-site 392
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FT /note= "putative"
FT Modified-site 448
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FT Modified-site 611
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 616
FT /label= N-linked_glycosylation_site
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FT Modified-site 624
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FT Modified-site 750
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Modified-site 816
FT /label= N-linked_glycosylation_site
FT /note= "putative"
FT Misc-difference 386
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
Gln at position 386"
FT Misc-difference 397
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
Gln at position 397"
FT Misc-difference 406
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
His at position 406"
FT Misc-difference 463
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
His at position 463"
XX W09317705-A.

PD 16-SEP-1993.
 XX
 PF 24-FEB-1993; 93WO-US01598.
 XX
 PR 13-MAR-1992; 92US-0850770.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Essex ME, Lee C, Lee T, Lee W;
 XX
 DR WPI; 1993-303140/38.
 XX
 PT Compsn. contg. selectively de-glycosylated HIV-1 envelope protein
 PT - shows improved protective immune response
 XX
 PS Claim 7; Page 15 and 23; 45pp; English.
 XX
 CC Mutant gp160 env protein C4 is specifically claimed. The
 CC amino acid sequence of the muten in does not appear in the
 CC specification; sequence R41025 has been derived from the HIV-1 HXB2
 CC isolate gp160 env sequence on the SWISS-PROT database (ID = ENV5HIV1X,
 CC Acc.#: P04578) and the description of C4 muten given in the
 CC specification. The combination of changes made to N-linked
 CC glycosylation sites in the C-terminal region of gp120 does not prevent
 CC viral infectivity but the resultant selective deglycosylation enables
 CC an immune response to be elicited by the muten.
 CC
 SQ Sequence 856 AA;
 Query Match 99.3%; Score 290; DB 14; Length 856;
 Best Local Similarity 98.1%; Pred. No. 6,1e-23;
 Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 NHTTWLEMDREINNTYSLIHSLIESONQOEKNEQELLDKRWASLMMWFI 52
 DB 624 NHTTWLEMDREINNTYSLIHSLIESONQOEKNEQELLDKRWASLMMWFI 675
 RESULT 10
 AAR41026
 ID AAR41026 standard; protein; 856 AA.
 AC AAR41026;
 XX
 DT 23-MAR-1994 (first entry)
 XX
 DE Selectively deglycosylated HIV-1 HXB2 env gp160 muten C5.
 XX
 KW N-linked glycosylation; gp120; human immunodeficiency virus; type 1;
 KW envelope glycoprotein; vaccine; site-directed mutagenesis.
 XX
 OS Human immunodeficiency virus type 1 (HXB2 strain).
 XX
 FH Key
 FH Peptide 1..30 Location/Qualifiers
 FT /label- signal_peptide
 FT 31..511
 FT /label- gp120
 FT /note- "exterior membrane glycoprotein"
 FT 512..856
 FT /label- gp41
 FT /note- "transmembrane glycoprotein"
 FT 88
 FT /label- N-linked_glycosylation_site
 FT /note- "putative"
 FT 136
 FT /label- N-linked_glycosylation_site
 FT /note- "putative"
 FT 141
 FT /label- N-linked_glycosylation_site
 FT /note- "putative"
 FT 156
 FT /label- N-linked_glycosylation_site
 FT Modified-site

FT Modified-site /note- "putative"
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 eliminated by substitution of Asn by
 Gln at position 386"

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 FT Modified-site 750
 FT /label- N-linked glycosylation_site
 FT /note- "putative"
 FT Modified-site 816
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 FT Misc-difference 386
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 386"
 FT Misc-difference 392
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 392"
 FT Misc-difference 397
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 397"
 FT Misc-difference 406
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 397"
 FT Misc-difference 448
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT His at position 406"
 FT Misc-difference 463
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT His at position 463"
 FT W09317705-A.
 FT 16-SEP-1993.
 FT PD 24-FEB-1993; 93WO-US01598.
 FT PR 13-MAR-1992; 92US-0850770.
 FT PA (HARD) HARVARD COLLEGE.
 FT PI Essex ME, Lee C, Lee T, Lee W;
 FT DR WPI; 1993-303140/38.
 FT XX Compsn. contg. selectively de-glycosylated HIV-1 envelope protein
 FT PT - shows improved protective immune response
 FT PS Claim 7; Page 15 and 23; 45pp; English.
 FT XX Mutant gp160 env protein C6 is specifically claimed. The
 FT CC amino acid sequence of the muten does not appear in the
 FT CC specification: sequence R41027 has been derived from the HIV-1 HXB2
 FT CC isolate gp160 env sequence on the SWISS-PROT database (ID - ENVSHYIX,
 FT CC Acc.#: P04576) and the description of C6 muten given in the
 FT CC specification. The combination of changes made to N-linked
 FT CC glycosylation sites in the C-terminal region of gp120 does not prevent
 FT CC viral infectivity but the resultant selective deglycosylation enables
 FT CC an immune response to be elicited by the muten.
 FT XX
 FT SQ Sequence 856 AA;

Query Match 99.3%; Score 290; DB 14; Length 856;
 Best Local Similarity 98.1%; Pred. No. 6.1e-23;
 Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLEESQNOEKNEQELLEDKRWASLWMTNFI 52
 DB 624 NHTTWLEMDREINNTSLIHSLEESQNOEKNEQELLEDKRWASLWMTNFI 675

RESULT 12
 ID AAR41028
 XX AAR41028 standard; protein; 856 AA.
 AC AAR41028;
 XX
 DT 23-MAR-1994 (first entry)
 XX
 DE Selectively deglycosylated HIV-1 HXB2 env gp160 muten Q.
 XX
 KW N-linked glycosylation; gp120; human immunodeficiency virus; type 1;
 KW envelope glycoprotein; vaccine; site directed mutagenesis.
 XX
 OS Human immunodeficiency virus type 1 (HXB2 strain).
 XX
 FH Key
 FH Peptide
 FT
 FT Protein
 FT
 FT Protein
 FT
 FT
 FT Location/Qualifiers
 FT 1..30
 FT /label- signal-peptide
 FT 31..511
 FT /label- gp120
 FT 512..856
 FT /note- "exterior membrane glycoprotein"
 FT /label- gp41
 FT /note- "transmembrane glycoprotein"
 FT 88
 FT /label- N-linked glycosylation_site
 FT /note- "putative"
 FT 136
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 FT 141
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 FT /note- "putative"
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 FT 301
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 FT /note- "putative"
 FT 392
 FT /label- N-linked glycosylation_site
 FT /note- "putative"
 FT 448
 FT Modified-site

FT	/label= N-linked glycosylation_site
FT	/note= "putative"
FT	Modified-site 611
FT	/label= N-linked glycosylation_site
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FT	Modified-site 616
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FT	/note= "putative"
FT	Modified-site 624
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FT	Modified-site 674
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FT	/note= "putative"
FT	Modified-site 750
FT	/label= N-linked glycosylation_site
FT	/note= "putative"
FT	Modified-site 816
FT	/label= N-linked glycosylation_site
FT	/note= "putative"
FT	Misc-difference 332
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by His at position 332"
FT	Misc-difference 339
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by Gln at position 339"
FT	Misc-difference 356
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by Gln at position 356"
FT	Misc-difference 386
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by Gln at position 386"
FT	Misc-difference 397
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by Gln at position 397"
FT	Misc-difference 406
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by His at position 406"
FT	Misc-difference 463
FT	/note= "putative N-linked glycosylation site eliminated by substitution of Asn by His at position 463"
XN	PW09J17705-A.
PN
XX	16-SEP-1993.
PD	.
XX	24-FEB-1993; 93WO-US01598.
PR	13-MAR-1992; 92US-0850770.
PA	(HARD) HARVARD COLLEGE.
PI	Essex ME, Lee C, Lee T, Lee W;
DRI	WTI; 1993-303140/38.
CC	- Compens. contg. selectively de-glycosylated HIV-1 envelope protein amino acid sequence of the mutlein does not appear in the mutant gp160 env protein Q is specifically claimed. The amino acid sequence of the mutlein does not appear in the Mutant gp160 env protein Q is specifically claimed. The amino acid sequence of the mutlein does not appear in the Claim 7; Page 18, 23 and 26; 45pp; English.

[illegible]

[illegible]

Wed May 7 14:34:24 2003

Search completed: May 7, 2003, 09:53:52
Job time : 49.4259 secs

us-09-877-606-3.rag

Page 13

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 17.5741 Seconds

(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-3

Perfect score: 292

Sequence: 1 NHTTWLEMDREINNTSLIHS.....NEQELLELDKWSLMMNFI 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277	94.9	851	2	env polypotein -
2	277	94.9	854	2	env polypotein - huma
3	277	94.9	856	1	env polypotein pr
4	277	94.9	861	1	env polypotein pr
5	268	91.8	856	1	env polypotein pr
6	260	89.0	358	1	env polypotein pr
7	254	87.0	856	1	env polypotein pr
8	253	86.6	861	1	env polypotein pr
9	250	85.6	443	2	env polypotein p
10	247	84.6	847	2	env polypotein p
11	247	84.6	847	2	env polypotein p
12	245	83.9	852	2	env polypotein p
13	244	83.6	357	2	env polypotein p
14	244	83.6	358	2	env polypotein p
15	244	83.6	358	2	env polypotein p
16	244	83.6	358	2	env polypotein p
17	242	82.9	859	1	env polypotein p
18	241	82.5	357	2	env polypotein p
19	241	82.5	357	2	env polypotein p
20	241	82.5	853	2	env polypotein p
21	241	82.5	855	1	env polypotein p
22	240	82.2	357	2	env polypotein p
23	238	81.5	852	1	env polypotein p
24	237	81.2	445	2	env polypotein p
25	236	80.8	729	1	env polypotein p
26	236	80.8	729	1	env polypotein p
27	236	80.8	861	1	env polypotein p
28	236	80.8	861	1	env polypotein p
29	234	80.1	846	1	env polypotein pr

30	233	79.8	868	1	VCLJH4	env polypotein -
31	232	79.5	843	1	H44001	env polypotein pr
32	229	78.4	859	2	T01672	env polypotein pr
33	228	78.1	136	2	JU0266	env polypotein pr
34	227	77.7	454	2	B41621	env polypotein D
35	223	76.4	136	2	JU0954	env polypotein D
36	213	72.9	357	2	S21990	env polypotein D
37	213	72.9	856	1	A44963	env polypotein pr
38	198	67.8	854	1	VCLJST	env polypotein pr
39	192	65.8	877	2	S49197	env polypotein pr
40	177	60.6	863	2	A53034	env polypotein p
41	130	44.5	151	2	S30448	env polypotein -
42	130	44.5	151	2	S30452	env polypotein - huma
43	130	44.5	151	2	S30451	env polypotein - huma
44	130	44.5	881	1	VCLJG3	env polypotein -
45	130	44.5	885	2	S04322	env polypotein -

ALIGNMENTS

RESULT 1

env polypotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlton, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199

C:Superfamily: type E retrovirus env polypotein

Query Match

Best Local Similarity 94.9%; Score 277; DB 2; Length 851;

Matches 49; Conservative 2; Mismatches 1; Indels 0;

Query Match

Best Local Similarity 94.2%; Score 277; DB 2; Length 854;

Matches 49; Conservative 2; Mismatches 1; Indels 0;

Query Match

Best Local Similarity 94.2%; Score 277; DB 2; Length 854;

Matches 49; Conservative 2; Mismatches 1; Indels 0;

Query Match

Best Local Similarity 94.2%; Score 277; DB 2; Length 854;

Matches 49; Conservative 2; Mismatches 1; Indels 0;

Query Match

Best Local Similarity 94.2%; Score 277; DB 2; Length 854;

Matches 49; Conservative 2; Mismatches 1; Indels 0;

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Retner, L.; Haseltine, W.; Patarca, R.; Liva, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Chrayef, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.9%; Score 277; DB 1; Length 856;
Best Local Similarity 94.2%; Pred. No. 6.5e-22;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 52
DB 624 NNMTEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 675
RESULT 4
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2961635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <WAI>
A:Cross-references: GB:K02013; NID:g326417; PIDN:AA59751.1; PID:g326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 94.9%; Score 277; DB 1; Length 861;
Best Local Similarity 94.2%; Pred. No. 6.5e-22;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 52
DB 629 NNMTEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 660
RESULT 5
VCLJLV
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Maesling, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laaky, L.A.; Capon, D.J
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <ME>
A:Cross-references: GB:K02083; NID:g555008; PIDN:AA59673.1; PID:g328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 91.8%; Score 268; DB 1; Length 856;
Best Local Similarity 90.4%; Pred. No. 6e-21;
Matches 47; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 52
DB 624 NNMTEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 675
RESULT 6
S21998
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STE1>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
C:Superfamily: type E retrovirus env polyprotein
Query Match 89.0%; Score 260; DB 2; Length 358;
Best Local Similarity 86.5%; Pred. No. 1.6e-20;
Matches 45; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 52
DB 126 NNMTEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNT 177
RESULT 7
VCLJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774

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A:Residues: 1-443 <NBR>
A:Cross-references: GB:I77230; NID:g328631; PIDN:AB03792.1; PID:g555015
A>Note: This virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:122-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/DomaIn: transmembrane #status predicted <TM>
F:9_23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:
OY      1 NHHTWLEMDREINNYTSLIHLSIESONQOEKNOELLELDKMASLNNWFNI 52
Db      364 NNMTWMEMERIDNYTSEIYTLIEESONQOEKNOELLELDKMASLNNWFPI 415

RESULT 10
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:U063632; NID:g1465777; PID:g1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match          84.6%; Score 247; DB 2; Length 847;
Best Local Similarity 82.7%; Pred. No. 1.le-18;
Matches 43; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY      1 NHHTWLEMDREINNYTSLIHLSIESONQOEKNOELLELDKMASLNNWFNI 52
Db      615 NNMTWMEMERIDNYTSEIYTLIEESONQOEKNOELLELDKMASLNNWFPI 666

RESULT 11
S13289
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13289
R'O'Brien, W.A.; Koyanagi, Y.; Namaze, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack,
Nature 348, 69-73, 1990
A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1
A:Reference number: S13288; MOLD:91043044; PMID:2172853
A:Accession: S13289
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OBR>
C:Superfamily: type E retrovirus env polyprotein

Query Match          84.6%; Score 247; DB 2; Length 847;
Best Local Similarity 82.7%; Pred. No. 1.le-18;
Matches 43; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY      1 NHHTWLEMDREINNYTSLIHLSIESONQOEKNOELLELDKMASLNNWFNI 52
Db      615 NNMTWMEMERIDNYTSEIYTLIEESONQOEKNOELLELDKMASLNNWFPI 666

```

RESULT 12

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: U12016
 R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
 AIDS Res. Hum. Retroviruses 14, 329-337, 1998
 A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in
 A:Reference numbers: Z17379; M0UD:96176716; PMID:9519894
 A:Accession: U12016
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-852 <MCC>
 A:Cross-references: EMBL:U09034; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polypotein


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FT DISULFID 385 418 BY SIMILARITY.
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 856 AA; 97212 MW; 66B16AB85107FED CRC64;

Query Match 99.3%; Score 290; DB 1; Length 856;
Best Local Similarity 98.1%; Pred. No. 2.3e-24;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESNOQOEKNEDELLEDKWASLWMEFI 52
DB 624 NHTTWLEMDREINNTSLIHSLSIESNOQOEKNEDELLEDKWASLWMEFI 675

RESULT 2
ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04624;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11707;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85228246; PubMed=2988795;
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
Shaw G.M., Wong-Staal F., Reddy E.P.;
RT "HIV-III env gene products synthesized in E. coli are recognized by
antibodies present in the sera of AIDS patients."
RL Cell 41:979-986(1985).
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

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DR EMBL: M14100; AAA44679.1; -.
DR HIV; M14100; ENVSHXB3.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.
FT CHAIN 1 30
FT CHAIN 1 511
FT CHAIN 512 856
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 296 331
FT DISULFID 378 445
FT DISULFID 385 418
FT CARBOHYD 88 136
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 856 AA; 97188 MW; 3373C68BB84C1AFC CRC64;

Query Match 99.3%; Score 290; DB 1; Length 856;
Best Local Similarity 98.1%; Pred. No. 2.3e-24;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESNOQOEKNEDELLEDKWASLWMEFI 52
DB 624 NHTTWLEMDREINNTSLIHSLSIESNOQOEKNEDELLEDKWASLWMEFI 675

RESULT 3
ENV_HV1H3 STANDARD; PRT; 856 AA.
AC Q70626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retrod viruses; Retroviridae; Lentivirus.

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Query Match	Score	DB	Length
99.3%	290	1	856
98.1%	Pre. No. 2.3e-24		

[illegible]

FT CARBOHD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 94.9%; Score 277; DB 1; Length 851;
 Best Local Similarity 94.2%; Pred. No. 6.2e-23;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNI 52
 DB 619 NNTWMEWDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNI 670

RESULT 5
 ENV_HY1B1 STANDARD; PRT; 856 AA.

AC P03375; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511123; PubMed=2578615;
 RA Kainer L., Haseltine W., Patarca R., Livak K.J., Starcich B.R., Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Pelletier S.R., Jr., Pearson M.L., Lattinberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C., Wong-Staal F.;
 RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RT Nature 313:277-284(1985).
 RL [2]
 RN DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RP MEDLINE=90285159; PubMed=2355006;
 RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;
 RA "Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells.";
 RT J. Biol. Chem. 265:10373-10382(1990).
 RL [3]
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 CC -----
 CC EMBL: M15654; AAA44205.1; -
 CC DR PIR: A03973; VCLJH3.
 CC DR HIV: M15654; ENVSBH102.
 CC InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120, 1.
 DR Pfam: PF00517; GP41, 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 512 856
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHD 88 88
 FT CARBOHD 136 136
 FT CARBOHD 141 141
 FT CARBOHD 156 156
 FT CARBOHD 160 160
 FT CARBOHD 186 186
 FT CARBOHD 197 197
 FT CARBOHD 230 230
 FT CARBOHD 234 234
 FT CARBOHD 241 241
 FT CARBOHD 262 262
 FT CARBOHD 276 276
 FT CARBOHD 289 289
 FT CARBOHD 295 295
 FT CARBOHD 301 301
 FT CARBOHD 332 332
 FT CARBOHD 339 339
 FT CARBOHD 356 356
 FT CARBOHD 386 386
 FT CARBOHD 392 392
 FT CARBOHD 397 397
 FT CARBOHD 406 406
 FT CARBOHD 448 448
 FT CARBOHD 463 463
 FT CARBOHD 611 611
 FT CARBOHD 616 616
 FT CARBOHD 625 625
 FT CARBOHD 637 637
 FT CARBOHD 674 674
 FT CARBOHD 750 750
 FT CARBOHD 816 816
 SQ SEQUENCE 856 AA; 97224 MW; 0BFFB1A18931BB27 CRC64;

Query Match 94.9%; Score 277; DB 1; Length 856;
 Best Local Similarity 94.2%; Pred. No. 6.2e-23;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNI 52
 DB 624 NNTWMEWDREINNTSLIHSIESONQOEKNEDELLEDKWASLWMMFNI 675

RESULT 6
 ENV_HY1B1 STANDARD; PRT; 861 AA.

AC P03377; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11686;
 RN [1]

FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 337789386f22ABA CRC64;

Query Match 93.8%; Score 274; DB 1; Length 853;
 Best Local Similarity 92.3%; Pred. No. 1,3e-22;
 Matches 48; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONOEKNEDELLELDKWSLWMPNI 52
 1:|||||
 DB 622 NNTWMEDEINNTSLIHSIESONOEKNEDELLELDKWSLWMPNI 673

RESULT 8
 ENV_HV1PV STANDARD: PRT: 856 AA.
 ID P03376;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 DE GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human Aids/Lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
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 CC -----
 CC EMBL: K02083; AAB59873.1; -
 DR EMBL: X01762; CAA25903.1; ALT_SEQ.
 DR PIR: A03974; VCLJVL.
 DR HIV: K02083; ENVSPV22.
 DR InterPro: IPR000328; Env_GP41;
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120.1.
 DR Pfam: PF00517; GP41.1.
 DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal.
 KW SIGNAL.
 FT CHAIN 1 30 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 31 511 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 512 856 BY SIMILARITY.
 FT DISULFID 54 74 BY SIMILARITY.
 FT DISULFID 119 205 BY SIMILARITY.
 FT DISULFID 126 196 BY SIMILARITY.
 FT DISULFID 131 157 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 228 239 BY SIMILARITY.

FT DISULFID 296 331 BY SIMILARITY.
 FT DISULFID 378 445 BY SIMILARITY.
 FT DISULFID 385 418 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MW; 5FCD1D03C1209B3 CRC64;

Query Match 91.8%; Score 268; DB 1; Length 856;
 Best Local Similarity 90.4%; Pred. No. 6.1e-22;
 Matches 47; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONOEKNEDELLELDKWSLWMPNI 52
 1:|||||
 DB 624 NNTWMEDEINNTSLIHSIESONOEKNEDELLELDKWSLWMPNI 675

RESULT 9
 ENV_HV1PV STANDARD: PRT: 856 AA.
 ID P31872;
 AC 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 DE GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=31678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86218077; PubMed=2423250;
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HIV-1/II/LAV, the retrovirus of AIDS.";
 RT Cell 45:637-648(1986).
 RL -1 MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INJECTED BY HER MOTHER.
 CC PIR: A24774; VCLJ3W.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.

DB 627 TWMEEREIDNTSLITLIESNQOEKNEDELLEDKMASLWMEFI 675

RESULT 11

ENV_HV1S3 STANDARD: PRT: 852 AA.

AC p19549; 1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11690;

RP MEDLINE=90317906; PubMed=2370688;

RX York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;

RA "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";

RT J. Virol. 64:4016-4020(1990).

RL

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CC

CC EMBL; M38427; AAA45067.1; -

DR HIV; M38427; ENV\$SEF12.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

RW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT SIGNAL 1 31 BY SIMILARITY.

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 297 331 BY SIMILARITY.

FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 129 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 852 AA; 96663 MM; EE/BF8D23C9910D CRC64;

SO SEQUENCE

Query Match 86.3%; Score 252; DB 1; Length 852;

Best Local Similarity 82.7%; Pred. No. 3.5e-20;

Matches 43; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESNQOEKNEDELLEDKMASLWMEFI 52

DB 620 NHTTWLEMDREINNTSLIHSIESNQOEKNEDELLEDKMASLWMEFI 671

RESULT 12

ENV_HV1S1 STANDARD: PRT: 847 AA.

AC p19550; 1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUN-1999 (Rel. 38, Last annotation update)

DE Envelope glycoprotein GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11691;

RP MEDLINE=90347835; PubMed=2384920.

RX Cheng-Mayer C., Guitroga M., Tung J.W., Dina D., Levy J.;

RA "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";

RT J. Virol. 64:4390-4398(1990).

RL

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CC

CC EMBL; M65024; AAA45072.1; -

DR HIV; M38428; ENV\$SEF162.

DR InterPro: IPR000328; Env.GP41.

DR InterPro: IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.

DR Pfam; PF00517; GP41; 1.

RW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT SIGNAL 1 29

FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 203 BY SIMILARITY.

FT DISULFID 125 194 BY SIMILARITY.

FT DISULFID 130 155 BY SIMILARITY.

FT DISULFID 216 245 BY SIMILARITY.

FT DISULFID 226 237 BY SIMILARITY.

FT DISULFID 294 328 BY SIMILARITY.

FT DISULFID 374 435 BY SIMILARITY.

FT DISULFID 381 408 BY SIMILARITY.

FT DISULFID 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CAROHD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 96135 MW; 0A901317ED7FE2AB CRC64;

Query Match 86.0%; Score 251; DB 1; Length 847;
 Best Local Similarity 82.7%; Pred. No. 4.3e-20;
 Matches 43; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTYSLHSIESONQOEKNEBELLFELDKWASIMWFI 52
 DB 615 NHTTLEMDREINNTYSLHSIESONQOEKNEBELLFELDKWASIMWFI 666

RESULT 13
 ENV_HV1W2 STANDARD; PRT; 847 AA.

AC P05880;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11705;
 [1]

RP MEDLINE=86235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or
 at risk for AIDS.";
 RL Science 232:1548-1553 (1986).

CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
 BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
 WAS PERINATALLY INFECTED BY HER MOTHER.

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 CC or send an email to license@sib-sib.ch).

DR EMBL: M12507; AAB12990.1; -
 DR HIV; M12507; ENVSMJ2.
 DR InterPro: IPR000328; ENV-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 CC Signal.

FT SIGNAL 1 29
 FT CHAIN 30 501
 FT CHAIN 502 847
 FT DISULFD 53 73
 FT DISULFD 118 202
 FT DISULFD 125 193
 FT DISULFD 130 152
 FT DISULFD 215 244
 FT DISULFD 225 236
 FT DISULFD 293 326
 FT DISULFD 372 435
 FT DISULFD 379 408
 FT CAROHD 87 87
 FT CAROHD 134 134
 FT CAROHD 140 140
 FT CAROHD 151 151
 FT CAROHD 155 155
 FT CAROHD 183 183
 FT CAROHD 184 184
 FT CAROHD 194 194
 FT CAROHD 231 231
 FT CAROHD 238 238
 FT CAROHD 259 259
 FT CAROHD 273 273
 FT CAROHD 286 286
 FT CAROHD 292 292
 FT CAROHD 327 327
 FT CAROHD 334 334
 FT CAROHD 350 350
 FT CAROHD 356 356
 FT CAROHD 380 380
 FT CAROHD 386 386
 FT CAROHD 390 390
 FT CAROHD 400 400
 FT CAROHD 438 438
 FT CAROHD 450 450
 FT CAROHD 602 602
 FT CAROHD 607 607
 FT CAROHD 616 616
 FT CAROHD 628 628
 SQ SEQUENCE 847 AA; 96466 MW; CD1E33D77AAB5CAE CRC64;

Query Match 83.2%; Score 243; DB 1; Length 847;
 Best Local Similarity 80.8%; Pred. No. 3.4e-19;
 Matches 42; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTYSLHSIESONQOEKNEBELLFELDKWASIMWFI 52
 DB 615 DNTLMEWEREIDNTYSLHSIESONQOEKNEBELLFELDKWASIMWFI 666

RESULT 14
 ENV_HV1MN STANDARD; PRT; 856 AA.

AC P05877;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.
 OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11696;
 [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=86219542; PubMed=3369091;
 RX Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates.";
 RL Virology 164:531-536 (1988).
 CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
 CC PATIENT IN 1984.

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 37.3148 seconds
(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-3

Perfect score: 292
Sequence: 1 NHTTWLEMDREINNTSLIH.....NEOELLELDKASLNMWENI 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	99.3	748	15	Q70606 human immun
2	290	99.3	752	15	Q70604 human immun
3	290	99.3	752	15	Q70605 human immun
4	286	97.9	747	15	Q70607 human immun
5	286	97.9	752	15	Q70608 human immun
6	285	97.6	856	15	Q90SM7 human immun
7	282	96.6	852	15	Q89J97 human immun
8	279	95.5	856	15	Q92877 simian-huma
9	277	94.9	645	15	Q993A6 human immun
10	277	94.9	851	15	Q78243 human immun
11	277	94.9	854	15	Q85382 human immun
12	277	94.9	856	15	Q72502 human immun
13	277	94.9	856	15	Q74599 human immun
14	277	94.9	856	15	Q74090 human immun
15	273	93.5	854	15	Q90178 human immun
16	273	93.5	854	15	Q78705 human immun

17	266	91.1	757	15	Q9q722 human immun
18	265	90.8	855	15	Q9e1R7 human immun
19	264	90.4	848	15	Q69990 human immun
20	263	90.1	851	15	Q56110 human immun
21	262	89.7	727	15	Q9q723 human immun
22	261	89.4	616	15	Q993B0 human immun
23	261	89.4	618	15	Q993B2 human immun
24	260	89.0	358	15	Q78120 human immun
25	260	89.0	848	15	Q69988 human immun
26	259	88.7	635	15	Q90U82 human immun
27	259	88.7	838	15	Q03806 human immun
28	259	88.7	852	15	Q69992 human immun
29	259	88.7	854	15	Q78225 human immun
30	259	88.7	855	15	Q03805 human immun
31	258	88.4	862	15	Q9E1S2 human immun
32	257	88.0	856	15	Q72993 human immun
33	257	88.0	859	15	Q80863 human immun
34	256	87.7	851	15	Q80852 human immun
35	256	87.7	863	15	Q9WU4 human immun
36	256	87.7	864	15	Q9YP48 human immun
37	255	87.3	847	15	Q69996 human immun
38	255	87.3	854	15	Q56112 human immun
39	255	87.3	863	15	Q9WU8 human immun
40	255	87.3	863	15	Q42031 human immun
41	255	87.3	864	15	Q9WU1 human immun
42	254	87.0	849	15	Q77368 human immun
43	253	86.6	847	15	Q91K06 human immun
44	253	86.6	847	15	Q41537 human immun
45	253	86.6	855	15	Q91K00 human immun

ALIGNMENTS

RESULT 1

ID Q70606 PRELIMINARY; PRT; 748 AA.
AC Q70606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B., Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB)."
RT AIDS Res. Hum. Retroviruses 10:1143-1153(1994).
RL [2]
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RX Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
RA Mulder K.E.;
RL EMBL; 012032; AAA76668.1; -;
DR InterPro; IPR000328; Env-GP1.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER
SQ SEQUENCE 748 AA; 84224 MW; 56BEDP186C67694B CRC64;

Query Match 99.3%; Score 290; DB 15; Length 748;
Best Local Similarity 98.1%; Pred. No. 1.6e-22;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 52
DB 620 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 671

RESULT 2
ID Q70604 PRELIMINARY: PRT; 752 AA.
AC Q70604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12030; AA76667.1; -
DR InterPro; IPR000328; Env-CP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match
Best Local Similarity 99.3%; Score 290; DB 15; Length 752;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 52
DB 624 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 675

RESULT 3
ID Q70605 PRELIMINARY: PRT; 752 AA.
AC Q70605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852;
GN
```

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RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12031; AA76667.1; -
DR InterPro; IPR000328; Env-CP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match
Best Local Similarity 99.3%; Score 290; DB 15; Length 752;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 52
DB 624 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 675

RESULT 4
ID Q70607 PRELIMINARY: PRT; 747 AA.
AC Q70607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
RA Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12034; AA76669.1; -
DR InterPro; IPR000328; Env-CP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match
Best Local Similarity 97.9%; Score 286; DB 15; Length 747;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 52
DB 619 NHTTWLEMDREINNTSLIHSIESQNOEKNEQELLELDKWSLWNNFNI 670

RESULT 5
ID Q70608 PRELIMINARY: PRT; 752 AA.
AC Q70608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN
```

OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)."
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12053; AAA76670.1; -;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KM AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
FT NON-TER
SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 97.9%; Score 286; DB 15; Length 752;
Best Local Similarity 98.1%; Pred. No. 4.2e-22;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWEMDREINNTSLHSLSIESQNOEKNEQELLEDKRWASIMWNT 52
DB 624 NHTTWEMDREINNTSLHSLSIESQNOEKNEQELLEDKRWASIMWNT 675

RESULT 6
OQ0SM7 PRELIMINARY; PRT; 856 AA.
AC OQ0SM7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HXB2;
RA Ataman-Onal Y., Cheynet V., Verrier B.;
RT "Mutations and transcriptional alterations associated with the
downregulation of HIV-1 envelope glycoprotein expression following
acute cytopathic effects."
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF358141; AAK49977.1; -;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KM AIDS: Coat protein; Glycoprotein; Polypotein; Transmembrane.
SQ SEQUENCE 856 AA; 97126 MW; 9458D02B2FD734B3 CRC64;

Query Match 97.6%; Score 285; DB 15; Length 856;
Best Local Similarity 96.2%; Pred. No. 6.1e-22;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWEMDREINNTSLHSLSIESQNOEKNEQELLEDKRWASIMWNT 52
DB 624 NHTTWEMDREINNTSLHSLSIESQNOEKNEQELLEDKRWASIMWNT 675

RESULT 7

OQ89797 PRELIMINARY; PRT; 852 AA.
ID OQ89797;
AC OQ89797;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM90-2;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
RT "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)."
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM90-2;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12053; AAA76685.1; -;
DR EMBL: U12036; AAA76671.1; -;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KM AIDS: Coat protein; Envelope protein; Glycoprotein; Polypotein;
Transmembrane.
SQ SEQUENCE 852 AA; 96347 MW; 4E865229D4E833CF CRC64;

Query Match 96.6%; Score 282; DB 15; Length 852;
Best Local Similarity 96.2%; Pred. No. 1.3e-21;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWEMDREINNTSLHSLSIESQNOEKNEQELLEDKRWASIMWNT 52
DB 620 NHTTWEMDREINNTSLHSLSIESQNOEKNEQELLEDKRWASIMWNT 671

RESULT 8
OQ2877 PRELIMINARY; PRT; 856 AA.
ID OQ2877;
AC OQ2877;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein.
GN ENV.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9908984; PubMed=9882298;
RX Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
Steenbeke T., Halloran M., Fenton J.W., Axelholm M.K., Letvin N.L.,
RA Sodroski J.G.;
RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
responsible for the pathogenicity of a multiply passaged simian-human
immunodeficiency virus (SHIV-HXB2)."
RL J. Virol. 73:976-984(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
Halloran M., Axelholm M.W., Letvin N.L., Sodroski J.G.;
RT Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF041850; AAD12142.1; -;
DR InterPro: IPR000328; Env_GP41.

```
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
DR AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97151 MM; C50BE0388FB73659 CRC64;

Query Match
Best Local Similarity 94.2%; Score 279; DB 15; Length 856;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLIHSIIIESNOQEKNEQLELDKMASTLWMMNT 52
DB 624 NMTWMEWDREINNTSLIHSIIIESNOQEKNEQLELDKMASTLWMMNT 675

RESULT 9
O993A6 PRELIMINARY; PRT; 645 AA.
AC O993A6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Truncated envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1007;
RX MEDLINE=21192672; PubMed=11287644;
RA Suman S., Lockey T.D., Slobod K.S., Jones B., Riberdy J.M.,
  White S.W., Doherty P.C., Hurwitz J.L.;
  "Localization of CD4+ T cell epitope hotspots to exposed strands of
  HIV envelope glycoprotein suggests structural influences on antigen
  processing.";
  RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).
  DR EMBL; AF321563; AAK18810.1; -
  DR InterPro: IPR000328; Env_GP41.
  DR InterPro: IPR000777; GP120.
  DR Pfam: PF00516; GP120; 1.
  DR Pfam: PF00517; GP41; 1.
  KW AIDS: Coat protein; Envelope protein; Glycoprotein; Polyprotein;
  Transmembrane.
  FT NON_TER 1
  SQ SEQUENCE 645 AA; 72485 MM; B076514BE93362EC CRC64;

Query Match
Best Local Similarity 94.9%; Score 277; DB 15; Length 645;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLIHSIIIESNOQEKNEQLELDKMASTLWMMNT 52
DB 593 NMTWMEWDREINNTSLIHSIIIESNOQEKNEQLELDKMASTLWMMNT 644

RESULT 10
O78243 PRELIMINARY; PRT; 851 AA.
AC O78243;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Env polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Carlini F., Federici M., Equestre M., Rloci S., Ratti G., Zibai O.,
  Verani P., Rossi G.B.;
  "Sequence analysis of HIV-1 proviral DNA from a non producer
```

```
RT Chronically infected HUT-78 cellular clone.";
RL J. Viral Diseases 1:40-55(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89352106; PubMed=2765297;
RA Federici M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
  Macchi B., Mangano N., Verani P., Rossi G.;
  "Biological and molecular characterization of producer and non
  producer clones from HUT-78 infected with a patient HIV isolate.";
  RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
  RN [3]
  RP SEQUENCE FROM N.A.
  RA Titti F., Federici M., Butto S., Orecchia A., Carlini F., Taddeo B.,
  Borsetti A., Saglio I., Verani P., Rossi G.;
  "Variability of HIV-1 virus: characteristics of an infected but not
  productive clone.";
  RL Int. J. Immunopharmacol. 3:17-23(1990).
  DR EMBL; Z11530; CA277628.1; -
  DR InterPro: IPR000328; Env_GP41.
  DR InterPro: IPR000777; GP120.
  DR Pfam: PF00516; GP120; 1.
  DR Pfam: PF00517; GP41; 1.
  KW AIDS: Coat protein; Glycoprotein; Polyprotein; Transmembrane.
  SQ SEQUENCE 851 AA; 96630 MM; 1A3767B987E98027 CRC64;

Query Match
Best Local Similarity 94.9%; Score 277; DB 15; Length 851;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLIHSIIIESNOQEKNEQLELDKMASTLWMMNT 52
DB 619 NMTWMEWDREINNTSLIHSIIIESNOQEKNEQLELDKMASTLWMMNT 670

RESULT 11
O85582 PRELIMINARY; PRT; 854 AA.
AC O85582;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86281827; PubMed=3016298;
RA Adechi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
  Martin M.A.;
  "Production of acquired immunodeficiency syndrome-associated
  retrovirus in human and nonhuman cells transfected with an infectious
  molecular clone.";
  RL J. Virol. 59:284-291(1986).
  RN [2]
  RP SEQUENCE FROM N.A.
  RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
  Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
  RN [3]
  RP SEQUENCE FROM N.A.
  RA Buckler C.E.;
  Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
  RL [4]
  RP SEQUENCE FROM N.A.
  RX MEDLINE=92219406; PubMed=1373204;
  RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
  "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
  gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T
  lymphocytes.";
  RL J. Virol. 66:3151-3154(1992).
  DR EMBL; M19921; AAA44992.1; -
  DR InterPro: IPR000328; Env_GP41.
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DR InterPro: IPR00777; GP120.
 DR Pfam: PF00517; GP41; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D595A CRC64;

Query Match
 Best Local Similarity 94.9%; Score 277; DB 15; Length 854;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 52
 DB 622 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 673

RESULT 12

OY 072502 PRELIMINARY; PRT; 854 AA.

AC 072502
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENV polyprotein.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

SEQUENCE FROM N.A.

RA MEDLINE-96036482; PubMed-7483282;
 RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
 Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
 RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
 from primary virus cultures using the polymerase chain reaction.";
 RL Virology 213:80-86(1995).

SEQUENCE FROM N.A.

RA MEDLINE-86281827; PubMed-3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
 Martin M.A.;

RT "Production of acquired immunodeficiency syndrome-associated
 retrovirus in human and nonhuman cells transfected with an infectious
 molecular clone.";

RL J. Virol. 59:284-291(1986).

DR EMBL: U26942; AAB60578.1; -;
 DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

RT CONFLICT 214 H -> L (IN REF. 2).
 FT CONFLICT 530 A -> S (IN REF. 2).
 FT CONFLICT 739 G -> D (IN REF. 2).

SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match
 Best Local Similarity 94.9%; Score 277; DB 15; Length 854;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 52
 DB 622 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 673

RESULT 13

OY 074599 PRELIMINARY; PRT; 856 AA.

AC 074599
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

SEQUENCE FROM N.A.

RA MEDLINE-90101366; PubMed-1688473;
 RA Cloyd M.W., Moore B.E.;

RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
 (HIV-1) Isolates.";

RL Virology 174:103-116(1990).

SEQUENCE FROM N.A.

RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: D86068; BAA12995.1; -;
 DR InterPro: IPR000328; Env_GP41.

DR Pfam: PF00517; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match
 Best Local Similarity 94.9%; Score 277; DB 15; Length 856;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 52
 DB 624 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 675

RESULT 14

OY 074090 PRELIMINARY; PRT; 856 AA.

AC 074090
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

ENV.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11676;

SEQUENCE FROM N.A.

RA MEDLINE-90101366; PubMed-1688473;
 RA Cloyd M.W., Moore B.E.;

RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
 (HIV-1) Isolates.";

RL Virology 174:103-116(1990).

SEQUENCE FROM N.A.

RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: D86069; BAA13003.1; -;
 DR InterPro: IPR000328; Env_GP41.

DR Pfam: PF00517; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.

SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match
 Best Local Similarity 94.9%; Score 277; DB 15; Length 856;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLSIESONQOEKNEQELLEDKMSLWMTNI 52

Db 624 NNMTEWMDREINNTSLIHSLIESQNOQEKNEQELLELDKWSLIMWNI 675

RESULT 15

ID 090178 PRELIMINARY; PRT: 854 AA.
 AC 090178;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074930; PubMed=7983770;
 RA Fang H., Pincus S.H.;
 RT "Unique insertion sequence and pattern of CD4 expression in variants
 RT selected with immunotoxins from human immunodeficiency virus type 1-
 RT infected T cells.";
 RL J. Virol. 69:75-81(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Fang H., Pincus S.H.;
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an
 RT immunotoxin-resistant variant T cell line.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF070521; AAC28452.1;
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 854 AA: 96885 MW: 0808F3AED27C693B CRC64;

Query Match 93.5%; Score 273; DB 15; Length 854;
 Best Local Similarity 92.3%; Pred. No. 1.1e-20;
 Matches 48; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLIESQNOQEKNEQELLELDKWSLIMWNI 52
 Db 622 NNMTEWMDREINNTSLIHSLIESQNOQEKNEQELLELDKWSLIMWNI 673

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 Job time : 39.3148 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 15.4074 Seconds

(without alignments)
99.302 Million cell updates/sec

Title: US-09-877-606-3

Perfect score: 292

Sequence: 1 NHTTWLEMDREINNTSLIHS.....NEDELEIDKWSLMMNFI 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCrus.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	290	99.3	138	4	US-09-570-921-21
3	290	99.3	138	4	US-09-570-921-22
4	290	99.3	138	4	US-09-570-921-23
5	290	99.3	138	4	US-09-570-921-24
6	290	99.3	138	4	US-09-570-921-25
7	290	99.3	138	4	US-09-570-921-26
8	290	99.3	138	4	US-09-570-921-27
9	290	99.3	138	4	US-09-570-921-28
10	290	99.3	138	4	US-09-570-921-29
11	290	99.3	138	4	US-09-570-921-30
12	290	99.3	138	4	US-09-570-921-31
13	290	99.3	138	4	US-09-570-921-32
14	290	99.3	138	4	US-09-570-921-33
15	290	99.3	138	4	US-09-570-921-34
16	290	99.3	138	4	US-09-570-921-35
17	290	99.3	138	4	US-09-570-921-36
18	290	99.3	138	4	US-09-570-921-37
19	290	99.3	138	4	US-09-570-921-38
20	290	99.3	138	4	US-09-570-921-39
21	290	99.3	138	4	US-09-570-921-40
22	290	99.3	138	4	US-09-570-921-41
23	290	99.3	138	4	US-09-570-921-42
24	290	99.3	138	4	US-09-570-921-43
25	290	99.3	138	4	US-09-570-921-44
26	290	99.3	138	4	US-09-570-921-45
27	290	99.3	138	4	US-09-570-921-46

28	277	94.9	338	4	US-08-474-349A-90	Sequence 90, Appl
29	277	94.9	338	4	US-08-255-208A-26	Sequence 26, Appl
30	277	94.9	345	4	US-08-817-441-49	Sequence 49, Appl
31	277	94.9	615	4	US-09-257-490-11	Sequence 11, Appl
32	277	94.9	826	2	US-08-375-510-2	Sequence 2, Appl
33	277	94.9	826	2	US-08-487-657-2	Sequence 2, Appl
34	277	94.9	839	4	US-08-472-240A-10	Sequence 10, Appl
35	277	94.9	854	4	US-09-309-572-23	Sequence 23, Appl
36	277	94.9	856	4	US-09-124-900-9	Sequence 9, Appl
37	277	94.9	861	1	US-08-127-499A-14	Sequence 14, Appl
38	277	94.9	861	1	US-08-482-847-14	Sequence 14, Appl
39	277	94.9	861	4	US-07-956-483-10	Sequence 10, Appl
40	277	94.9	861	4	US-07-956-483-16	Sequence 16, Appl
41	277	94.9	861	4	US-08-472-240A-1	Sequence 1, Appl
42	277	94.9	861	4	US-08-472-240A-7	Sequence 7, Appl
43	277	94.9	861	4	US-08-817-441-103	Sequence 103, App
44	277	94.9	863	3	US-08-463-210-11	Sequence 11, Appl
45	277	94.9	880	2	US-08-788-815-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-09-570-921-20
Sequence 20, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT FILING DATE: US/09/570,921
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 20
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-20

Query Match 99.3% Score 290; DB 4; Length 138;
Best Local Similarity 98.1%; Pred. No. 5.3e-26;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEDELEIDKWSLMMNFI 52
DB 85 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEDELEIDKWSLMMNFI 136

RESULT 2
US-09-570-921-21
Sequence 21, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT FILING DATE: US/09/570,921
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 21
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QY 1 NHTTWMDEINNTSLHSLEESONOEKNEQELLEIDKASLMMWNI 52
DB 420 NHTTWMDEINNTSLHSLEESONOEKNEQELLEIDKASLMMWNI 471

RESULT 6

US-08-444-882-8
Sequence 8, Application US/08444882
Patent No. 5622705
GENERAL INFORMATION:
APPLICANT: Morrow, Casey D.
TITLE OF INVENTION: ENCAPSIDATED POLIOVIRUS NUCLEIC
ACID AND METHODS OF MAKING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,882
FILING DATE: 19-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:
NAME: Geary III, William C.
REGISTRATION NUMBER: 31,359
REFERENCE/DOCKET NUMBER: UAG-004
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-444-882-8

Query Match 99.3%; Score 290; DB 1; Length 519;
Best Local Similarity 98.1%; Pred. No. 2.4e-25;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWMDEINNTSLHSLEESONOEKNEQELLEIDKASLMMWNI 52
DB 420 NHTTWMDEINNTSLHSLEESONOEKNEQELLEIDKASLMMWNI 471

RESULT 7

US-08-389-459A-8
Sequence 8, Application US/08389459A
Patent No. 5817512
GENERAL INFORMATION:
APPLICANT: Morrow, Casey D. and Porter, Donna, C.
TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
NUCLEIC ACID AND METHODS OF MAKING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS

US-08-389-459A-8

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,459A
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silverl, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: UAG-004CP
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-389-459A-8
Query Match 99.3%; Score 290; DB 2; Length 519;
Best Local Similarity 98.1%; Pred. No. 2.4e-25;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWMDEINNTSLHSLEESONOEKNEQELLEIDKASLMMWNI 52
DB 420 NHTTWMDEINNTSLHSLEESONOEKNEQELLEIDKASLMMWNI 471

RESULT 8

US-08-987-867A-8
Sequence 8, Application US/08987867A
Patent No. 6063384
GENERAL INFORMATION:
APPLICANT: C. Morrow et al.
TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
NUCLEIC ACID AND METHODS OF MAKING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,867A
FILING DATE: 09-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: UAG-004CPDV
TELECOMMUNICATION INFORMATION:

US-08-987-867A-8

TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-987-867A-8

Query Match 99.3%; Score 290; DB 3; Length 519;
Best Local Similarity 98.1%; Pred. No. 2.4e-25;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 52
DB 420 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 471

RESULT 9

US-07-916-098A-2
Sequence 2, Application US/07916098A
Patent No. 5871732

GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916, 098A
CLASSIFICATION: 424
FILING DATE: July 24, 1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991

CLASSIFICATION: 424
APPLICATION NUMBER: 07/618, 542
FILING DATE: No. 5871732ember 27, 1990

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL

REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234

TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 856 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-916-098A-2

Query Match 99.3%; Score 290; DB 2; Length 856;
Best Local Similarity 98.1%; Pred. No. 4.3e-25;

Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 52
DB 624 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 675

RESULT 10

US-09-337-387-11
Sequence 11, Application US/09337387
Patent No. 6420545

GENERAL INFORMATION:
APPLICANT: HOXIE, James A.
APPLICANT: LABRANCHE, Celia C.
APPLICANT: DOMS, Robert W.
APPLICANT: HOFFMAN, Trevor L.
TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND
TITLE OF INVENTION: THERAPEUTICS
FILE REFERENCE: HOXIE 9596-10401 (0282)
CURRENT APPLICATION NUMBER: US/09/337,387
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/317,556
PRIOR FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11

LENGTH: 856
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-337-387-11

Query Match 99.3%; Score 290; DB 4; Length 856;
Best Local Similarity 98.1%; Pred. No. 4.3e-25;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 52
DB 624 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 675

RESULT 11

US-09-570-921-22
Sequence 22, Application US/09570921
Patent No. 6455265

GENERAL INFORMATION:
APPLICANT: SERIES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921

CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447

PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387

PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22

LENGTH: 138
TYPE: PRT

ORGANISM: Human
US-09-570-921-22

Query Match 94.9%; Score 277; DB 4; Length 138;
Best Local Similarity 94.2%; Pred. No. 1.6e-24;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 52
DB 85 NHTTWLEMDREINNTYSLIHSLSIESQNOOEKNEQELLEDKWSLWNNFNI 136

RESULT 12

Db 5 NNMWMEWDREINNTSLIHSLIESQNOQEKNEQELLELDKRWASIMNNTI 56

Search completed: May 7, 2003, 09:59:49
Job time : 17.4074 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 28.6481 Seconds

(without alignments)
167.038 Million cell updates/sec

Title: US-09-877-606-3

Perfect score: 292
Sequence: 1 NHTTWLEMDREINNYTSLIR.....NEOELLIDKXWASIMNWFNI 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PC1_NEM_PUB pep: *
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13: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB pep: *
14: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	290	99.3	268 10 US-09-854-816-16	Sequence 16, Appl
2	290	99.3	344 9 US-10-040-349B-1	Sequence 1, Appl1
3	290	99.3	519 10 US-09-756-551A-8	Sequence 8, Appl1
4	290	99.3	856 10 US-09-476-242-1	Sequence 1, Appl1
5	277	94.9	56 10 US-09-779-451-4	Sequence 4, Appl1
6	277	94.9	177 9 US-10-040-349B-2	Sequence 2, Appl1
7	277	94.9	221 9 US-10-059-271-84	Sequence 84, Appl1
8	277	94.9	232 9 US-10-059-271-81	Sequence 81, Appl1
9	277	94.9	254 9 US-10-059-271-82	Sequence 82, Appl1
10	277	94.9	256 9 US-10-059-271-97	Sequence 97, Appl1
11	277	94.9	268 10 US-09-854-816-17	Sequence 17, Appl1
12	277	94.9	345 10 US-09-854-816-18	Sequence 16, Appl1
13	277	94.9	345 10 US-10-026-741-49	Sequence 49, Appl1
14	277	94.9	345 10 US-09-779-451-8	Sequence 8, Appl1
15	277	94.9	391 9 US-10-059-271-93	Sequence 93, Appl1
16	277	94.9	853 9 US-10-003-035-33	Sequence 33, Appl1
17	277	94.9	861 9 US-10-026-741-103	Sequence 103, Appl1
18	277	94.9	1101 9 US-10-003-035-53	Sequence 53, Appl1
19	277	94.9	1186 9 US-10-003-035-55	Sequence 55, Appl1

20	274	93.8	268 10 US-09-854-816-19	Sequence 19, Appl1
21	260	89.0	269 10 US-09-854-816-46	Sequence 46, Appl1
22	259	88.7	268 10 US-09-854-816-13	Sequence 13, Appl1
23	256	87.7	46 10 US-09-779-451-41	Sequence 41, Appl1
24	255	87.3	269 10 US-09-854-816-43	Sequence 43, Appl1
25	254	87.0	268 10 US-09-854-816-9	Sequence 9, Appl1
26	253	86.6	269 10 US-09-854-816-12	Sequence 12, Appl1
27	252	86.3	269 10 US-09-854-816-28	Sequence 28, Appl1
28	251	86.0	268 10 US-09-854-816-26	Sequence 26, Appl1
29	251	86.0	619 10 US-09-891-609-4	Sequence 4, Appl1
30	251	86.0	646 10 US-09-891-609-2	Sequence 2, Appl1
31	251	86.0	847 10 US-09-476-242-2	Sequence 2, Appl1
32	250	85.6	269 10 US-09-854-816-50	Sequence 50, Appl1
33	248	84.9	269 10 US-09-854-816-44	Sequence 44, Appl1
34	247	84.6	268 10 US-09-854-816-8	Sequence 8, Appl1
35	247	84.6	579 9 US-10-032-162-15	Sequence 15, Appl1
36	247	84.6	625 9 US-10-032-162-17	Sequence 17, Appl1
37	247	84.6	643 9 US-10-032-162-13	Sequence 13, Appl1
38	246	84.2	268 10 US-09-854-816-41	Sequence 41, Appl1
39	243	83.2	267 10 US-09-854-816-38	Sequence 38, Appl1
40	243	83.2	269 10 US-09-854-816-32	Sequence 32, Appl1
41	243	83.2	269 10 US-09-854-816-34	Sequence 34, Appl1
42	243	83.2	269 10 US-09-854-816-45	Sequence 45, Appl1
43	242	82.9	267 10 US-09-854-816-15	Sequence 15, Appl1
44	242	82.9	269 10 US-09-854-816-6	Sequence 6, Appl1
45	241	82.5	267 10 US-09-854-816-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-09-854-816-16

Sequence 16, Application US/09854816
Patent No. US20020151473A1

GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovashnik
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatlin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD, Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P100582

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/552-9881

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-854-816-16

Query Match 99.3%; Score 290; DB 10; Length 268;
Best Local Similarity 98.1%; Pred. No. 1.3e-24;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 52
DB 154 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 205

RESULT 2
US-10-040-349B-1
Sequence 1, Application US/10040349B
Publication No. US20030082521A1

GENERAL INFORMATION:
APPLICANT: Brasseur, Robert
APPLICANT: Charloleaux, Benoit
APPLICANT: Chevalier, Michel
APPLICANT: El Habib, Raphaelle
APPLICANT: Krell, Tino
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
FILE REFERENCE: 01-078-A
CURRENT APPLICATION NUMBER: US/10/040.349B
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0

SEQ ID NO 1
LENGTH: 344
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
NAME/KEY: Peptide
LOCATION: (1)..(344)
OTHER INFORMATION: gp41 LAI protein
US-10-040-349B-1

Query Match 99.3%; Score 290; DB 9; Length 344;
Best Local Similarity 98.1%; Pred. No. 1.8e-24;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 52
DB 113 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 164

RESULT 3
US-09-756-551A-8
Sequence 8, Application US/09756551A
Patent No. US20020051768A1

GENERAL INFORMATION:
APPLICANT: C. Morrow et al.
TITLE OF INVENTION: ENCAPSATED RECOMBINANT VIRAL
TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/756.551A
FILING DATE: 08-JAN-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/376,184
FILING DATE: 17-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,867
FILING DATE: 09-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/389,459
FILING DATE: 15-FEB-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lauro, Peter C.
REGISTRATION NUMBER: 32,360
REFERENCE/DOCKET NUMBER: UAI-004CPDVZCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-756-551A-8

Query Match 99.3%; Score 290; DB 10; Length 519;
Best Local Similarity 98.1%; Pred. No. 2.8e-24;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 52
DB 420 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 471

RESULT 4
US-09-476-242-1
Sequence 1, Application US/09476242
Patent No. US20020146683A1

GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: HARROG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476.242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 856
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-476-242-1

Query Match 99.3%; Score 290; DB 10; Length 856;
Best Local Similarity 98.1%; Pred. No. 4.8e-24;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 52
DB 624 NHTTWLEMDREINNTSLIHSLSIESONQOEKNEQELLELDKWSLWVFN 675

RESULT 5
US-09-779-451-4
Sequence 4, Application US/09779451

Patent No. US20020094521A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
US-09-779-451-4

Query Match 94.9%; Score 277; DB 10; Length 56;
Best Local Similarity 94.2%; Pred. No. 6.4e-24;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 52
1:|||||
DB 2 NNMWTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 53

RESULT 6
US-10-040-349B-2
Sequence 2, Application US/10040349B
Publication No. US20030082521A1
GENERAL INFORMATION:
APPLICANT: Brasseur, Robert
APPLICANT: Charleaux, Benoit
APPLICANT: Chevallier, Michel
APPLICANT: El Habib, Ranaelle
APPLICANT: Krell, Tino
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
FILE REFERENCE: 01-078-A
CURRENT APPLICATION NUMBER: US/10/040,349B
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 177
TYPE: PRT
ORGANISM: Human Immunodeficiency virus type 1
FEATURE:
NAME/KEY: Peptide
LOCATION: (1)..(177)
OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2

Query Match 94.9%; Score 277; DB 9; Length 177;
Best Local Similarity 94.2%; Pred. No. 2.3e-23;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 52
1:|||||
DB 90 NNMWTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 141

RESULT 7
US-10-059-271-84
Sequence 84, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

TITLE OF INVENTION: BEING IMMOBILIZED
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
LENGTH: 221
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84

Query Match 94.9%; Score 277; DB 9; Length 221;
Best Local Similarity 94.2%; Pred. No. 2.9e-23;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 52
1:|||||
DB 117 NNMWTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 168

RESULT 8
US-10-059-271-81
Sequence 81, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: BEING IMMOBILIZED
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 232
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-81

Query Match 94.9%; Score 277; DB 9; Length 232;
Best Local Similarity 94.2%; Pred. No. 3.1e-23;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 52
1:|||||
DB 130 NNMWTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKWSIMWPNFI 181

RESULT 9
US-10-059-271-82
Sequence 82, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271

```

:
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: DE 101 06 295
: PRIOR FILING DATE: 2001-02-02
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 82
: LENGTH: 254
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: peptide
US-10-059-271-82

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Query Match	94.98;	Score 277;	DB 9;	Length 254;
Best Local Similarity	94.28;	Pred. No.	3.4e-23;	
Matches 49;	Conservative	2;	Mismatches 1;	Indels 0;
				Gaps 0;

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QY      1 NHTWLEWMDREINNTSLIHSIESQNOQEKNEDELLELDKWSLWNNFI 52
      11 : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      152 NNMWTMEWMDREINNTSLIHSIESQNOQEKNEDELLELDKWSLWNNFI 203
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RESULT 10
US-10-059-271-97
: Sequence 97, Application US/10059271
: Publication No. US20030082208a1
: GENERAL INFORMATION:
: APPLICANT: REPKE, HEINRICH
: APPLICANT: BUDE, ECKHARD
: APPLICANT: NICOLAUS, STEFAN
: TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
: TITLE OF INVENTION: BEING IMMOBILIZED
: FILE REFERENCE: ALBRE-22
: CURRENT APPLICATION NUMBER: US/10/059,271
: CURRENT FILING DATE: 2002-01-31
: PRIOR APPLICATION NUMBER: DE 101 06 295
: PRIOR FILING DATE: 2001-02-02
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 97
: LENGTH: 256
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: OTHER INFORMATION: peptide
US-10-059-271-97

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Query Match 94.9%; Score 277; DB 9; Length 256;
Best Local Similarity 94.2%; Pred. No. 3,4e-23;
Matches 49; Conservative 2; Mismatches 1; Indels
0; Gaps 0;

QY 1 NHTTWELENDRELNNTTSLSHSLESNOOQEENBELLFLDKMASLWNNFTI 52
+ :
Db 152 NNMTWMEDRELNNTTSLSHSLESNOOQEENBELLFLDKMASLWNNFTI 203

QY 1 NHTWLEWDREINNTSLIHSLIEESQNQEKNQELLELDKASLWNFNI 52
1 : :::
Db 152 NNKTWMEWDREINNTSLIHSLIEESQNQEKNQELLELDKASLWNFNI 203

RESULT 11
 US-09-854-816-17
 : Sequence 17, Application US/09854816
 : Patent No. US20020151473A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Andrew C. Braisted
 :
 : J. Kevin Judice
 :
 : Robert S. McDowell
 : J. Christopher Phelan
 : Melissa A. Starovasinik
 : James A. Wells
 :
 : TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 : Making Same
 :
 : NUMBER OF SEQUENCES: 113
 :
 : CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA: 100/001-015

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1 INFORMATION FOR SEQ ID NO: 17:
2
3 SEQUENCE CHARACTERISTICS:
4
5 LENGTH: 268 amino acids
6
7 type: Amino Acid
8
9 TOPOLOGY: Linear
10
11 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
12
13 US-09-854-816-17

```

US-09-854-816-17

	Query Match	Score	DB 10;	Length
Best Local Similarity	94.9%;	277;	268;	
Matches	49;	Pred. No. 3.6e-23;		
	Conservative	2;	Mismatches	1;
			Indels	0;
			Gaps	0;

QY **1** NHTTWLEMDREINNTYSLIHSLIESQNQEKNQELLEDKVASLMWNFI 52
 | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db **154** NNMTWMEWDREINNTYSLIHSLIESQNQEKNQELLEDKVASLMWNFI 205

RESULT 12
 US-09-854-816-18
 : Sequence 18. Application US/09854816
 Patent No. US20020151473A1
 GENERAL INFORMATION:
 APPLICANT: Andrew C. Braisted
 J. Kevin Judice
 Robert S. McDowell
 J. Christopher Phelan
 Melissa A. Starovasanik
 James A. Wells
 TITLE OF INVENTION: Constrained Helical Peptides and Methods of
 Making Same
 NUMBER OF SEQUENCES: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatlin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/854,816
 FILING DATE: 15-May-2001
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-854-816-18

Query Match 94.9%; Score 277; DB 10; Length 268;
Best Local Similarity 94.2%; Pred. No. 3.6e-23;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKASIMWNT 52
1:|||||
DB 134 NMTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKASIMWNT 205

RESULT 13
US-10-026-741-49
Sequence 49, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDRE
OUILLENT, CAROLINE
GUERARD, DENISE
MONTAGNER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JAOUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260, 6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-026-741-49

Query Match 94.9%; Score 277; DB 9; Length 345;
Best Local Similarity 94.2%; Pred. No. 4.8e-23;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKASIMWNT 52
1:|||||
DB 113 NMTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKASIMWNT 164

RESULT 14
US-09-779-451-8
Sequence 8, Application US/09779451
Patent No. US20020094521A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 345
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-8

Query Match 94.9%; Score 277; DB 10; Length 345;
Best Local Similarity 94.2%; Pred. No. 4.8e-23;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOEKNEQELLELDKASIMWNT 52
1:|||||
DB 113 NMTWMDREINNTSLIHSLSIESQNOEKNEQELLELDKASIMWNT 164

RESULT 15
US-10-059-271-93
Sequence 93, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPE, HEINRICH
BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
LENGTH: 391
TYPE: PRT
ORGANISM: Artificial Sequence

Wed May 7 14:34:25 2003

us-09-877-606-3.rapb

Page 6

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:   FEATURE:      Description of Artificial Sequence: Synthetic
:   OTHER INFORMATION:
:   ;
:   ;   OTHER INFORMATION:      peptide
:   ;
:   US-10-059-271-93

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Query Match	94.98;	Score 277;	DB 9;	Length 391;
Best Local Similarity	-94.28;	Pred. No. 5.5e-23;		
Matches	49;	Conservative	2;	Mismatches 1;
				Indels 0;
				Gaps 0;

OY 1 NHTTWLEWDREINNYTSLIHSLIEESQNOOEKNBQELLELDKWSLWNWNTI 52
 | : ::::::::::::::::::::|
Db 155 NNMTMWEWDREINNYTSLIHSLIEESQNOOEKNBQELLELDKWSLWNWNTI 206

Search completed: May 7, 2003, 10:21:53
Job time : 29.6481 secs

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1960	8.0	8.0
1970	9.0	9.0
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2000	12.0	15.0
2010	13.0	17.0
2020	14.0	19.0
2030	15.0	20.0
2040	16.0	20.0
2050	17.0	20.0

PT Production of constrained helical peptide(s) by linking side chains
PT on termini of octa-peptide - derived from human immunodeficiency
PT virus gp41 protein, useful in vaccines for treatment and prevention
PT of infection
XX
PS Claim 11; Page 156; 279pp; English.
XX
CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins
CC of known HIV virus strains (AAY22871, AAY22880, AAY22888 and
CC AAY22903 represent consensus sequences of various sections of the gp41
CC protein). Sequences derived from the peptides are used to produce
CC constrained helical peptides of the invention. The constrained helical
CC peptide is produced by synthesizing an octapeptide in which both terminal
CC amino acids have a side-chain that includes a group able to form an amide
CC bond, and cyclizing the octapeptide by reacting the specified side-chain
CC residues with a difunctional linker to produce two amide bonds.
CC The constrained helical peptides are used to treat or prevent HIV
CC infection, especially as vaccines that generate antibodies that
CC prevent viral membrane fusion or infectivity. Vaccines may contain
CC constrained helical peptides derived from several different strains of
CC HIV. The antibodies are also useful for diagnosing HIV infection. Other
CC uses for the constrained helical peptides are in affinity purification
CC of ligands (particularly where complete binding protein is not readily
CC available, e.g. replacements for protein A in immunoglobulin
CC purification); as epitope mimics for antibody production; for isolation
CC of synthetic antibody clones from phage display libraries, or as stable
CC forms of "floppy" peptides or proteins.
XX
SQ Sequence 268 AA;
XX
Query Match 64.2%; Score 290; DB 19; Length 268;
Best Local Similarity 98.1%; Pred. No. 1.4e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOQEKNEDELIDKMASLWNPNI 52
DB 154 NHTTWLEMDREINNTSLIHSLSIESQNOQEKNEDELIDKMASLWNPNI 205
XX
RESULT 2
ABG68291
ID ABG68291 standard; Protein: 268 AA.
XX
AC ABG68291;
XX
DT 07-OCT-2002 (first entry)
XX
DE Envelope protein gp41 from HIV clade B strain #10.
XX
KW HIV; glycoprotein; gp41; antigen; helical conformation;
KW virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
KW viral envelope protein; vaccine; virucide; anti-HIV.
XX
OS Human immunodeficiency virus type 1 clade B.
XX
XX US6271198-B1.
XX
PN 07-AUG-2001.
XX
PD 05-NOV-1997; 97US-0965056.
XX
PE 16-JUN-1997; 97US-049787P.
XX
PR 06-NOV-1996; 96US-0743698.
XX
PR 16-JUN-1997; 97US-0876698.
XX
PA (GETH) GENENTECH INC.
XX
XX Braisted AC, Judice JK, McDowell RS, Phelan JC, Starovasnik MA;
XX Wells JA;
XX WPI; 2002-487624/52.
XX

PT New cyclic peptides from human immune deficiency virus gp41, useful for
PT treatment or prevention of HIV infection, are constrained to have
PT alpha-helical conformation -
XX
PS Disclosure; Column 151-154; 175pp; English.
XX
CC The invention relates to cyclic peptides (A) with a constrained helical
CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
CC protein) of human immunodeficiency virus (HIV). The cyclic
CC peptides have formulas given in the specification part of which are
CC C, D, E or O. The peptides are used to cause induction of a specific
CC immune response, resulting in antibodies that prevent virus-induced
CC membrane fusion. The peptides are used to treat subjects with, or at risk
CC of, HIV infection, either as antifusion/anti-infection agents or,
CC preferably where associated with a carrier, as an immunogen (including as
CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
CC cases of health care accidents. The peptides can be based on specific HIV
CC strains, e.g. breakthrough isolates of HIV that have developed during
CC vaccine trials, so a combination of them should cover a wide range of
CC protection. The present sequence is gp41 protein from a particular
CC HIV clade used to derive a consensus sequence of gp41.
XX
SQ Sequence 268 AA;
XX
Query Match 64.2%; Score 290; DB 23; Length 268;
Best Local Similarity 98.1%; Pred. No. 1.4e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTSLIHSLSIESQNOQEKNEDELIDKMASLWNPNI 52
DB 154 NHTTWLEMDREINNTSLIHSLSIESQNOQEKNEDELIDKMASLWNPNI 205
XX
RESULT 3
ABB83400
ID ABB83400 standard; Protein: 344 AA.
XX
AC ABB83400;
XX
DT 19-SEP-2002 (first entry)
XX
DE HIV gp41 LAI protein #1.
XX
KW HIV; gp41; LAI; virucide; anti-HIV; vaccine; HIV infection.
XX
OS Human immunodeficiency virus.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..23
XX FT Peptide /label= Fusion_peptide
XX FT Domain 173..194
XX FT /label= Transmembrane_domain
XX
XX WO200253587-A2.
XX
PN 11-JUL-2002.
XX
PD 04-JAN-2002; 2002WO-FR00031.
XX
PE 05-JAN-2001; 2001FR-0000141.
XX
PR 23-JAN-2001; 2001FR-0000848.
XX
PA (AVER) AVENTIS PASTEUR.
XX
XX Brasseur R, Charlotiaux B, Chevallier M, El Habib R, Kreil T;
XX Sodoyer R;
XX WPI; 2002-528852/56.
XX
XX New mutant human immune deficiency virus gp41 polypeptide, useful in
PT

PT vaccines against human immune deficiency virus, makes the intermediate
PT state of the native polypeptide
XX
PS Disclosure; Page 29; 29pp; French.
XX
CC The present invention relates to novel mutant HIV gp41 LAI proteins
CC (AB83411-AB83420). The mutants can form a structure corresponding to,
CC or mimicking, the intermediate state of gp41. The mutants, or their
CC conjugate with a carrier, or vectors containing nucleic acid that encode
CC them, are used in vaccines for treatment or prevention of infection by
CC HIV. The present sequence is wild-type HIV gp41 LAI protein, which
CC was used to generate the mutants of the invention.
XX
SQ Sequence 344 AA;
XX
Query Match 64.2%; Score 290; DB 23; Length 344;
Best Local Similarity 98.1%; Pred. No. 1.9e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHTTWLEMDREINNTYSLHSLIEESONOEKNEDELLELDKWSLMMNFI 52
DB 113 NHTTWLEMDREINNTYSLHSLIEESONOEKNEDELLELDKWSLMMNFI 164
XX
RESULT 4
AAR53785
ID AAR53785 standard; Protein; 420 AA.
XX
AC AAR53785;
XX
DT 28-DEC-1994 (first entry)
XX
DE Translation of HIV-1 in the region encoding the gp41 polypeptide.
XX
KM Human immunodeficiency virus; HIV-1; AIDS; lentivirus; TM protein;
XX extracellular protein; transmembrane protein; gp41.
XX
OS HIV-1.
XX
FH Key
FT Protein 43.387
FT Location/Qualifiers
FT /label= gp41
XX
PN WO9412533-A.
XX
PD 09-JUN-1994.
XX
PF 12-JAN-1993; 93MO-US00212.
XX
PR 23-NOV-1992; 9205-0979975.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Essex ME, Lee TH, Yu X;
XX
DR WPI: 1994-200197/24.
DR N-PSDB: AA066275.
XX
PT Method for treating HIV patients - comprises administration of
PT mutated gp41 polypeptide
XX
PS Claim 11; Fig 1; 54pp; English.
XX
CC The inventors claim a method of treating a patient infected with HIV
CC by administering a mutated gp41 polypeptide or a therapeutic
CC composition comprising nucleic acid encoding the mutant gp41
CC polypeptide in an expressible genetic construction. The mutant gp41
CC polypeptide contains a deletion of at least one AA in at least one
CC of the following regions of wild type gp41 (AAR53783): AAs 844-856;
CC 814-856; 796-856; 776-856; 753-856; or 710-856, effective to either
CC disrupt viral replication or HIV or disrupt the assembly of viral
CC Env proteins in an HIV infected cell. AA066275 corresponds to Dps 7631-
CC 8890 of wt HIV-1. X in the AA sequence represents the posn. of a

CC stop codon in AA066275.
XX
SQ Sequence 420 AA;
XX
Query Match 64.2%; Score 290; DB 15; Length 420;
Best Local Similarity 98.1%; Pred. No. 2.4e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHTTWLEMDREINNTYSLHSLIEESONOEKNEDELLELDKWSLMMNFI 52
DB 155 NHTTWLEMDREINNTYSLHSLIEESONOEKNEDELLELDKWSLMMNFI 206
XX
RESULT 5
AAM00181
ID AAM00181 standard; Protein; 519 AA.
XX
AC AAM00181;
XX
DT 12-NOV-1996 (first entry)
XX
DE HIV-1 env protein.
XX
KM Poliovirus; encapsidation; capsid; vaccine; genetic immunisation;
XX HIV-1; human immunodeficiency virus type 1; env protein.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9625173-A1.
XX
PD 22-AUG-1996.
XX
PF 13-FEB-1996; 96MO-US01895.
XX
PR 15-FEB-1995; 95US-0389459.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Ansardl DC, Morrow CD, Porter DC;
XX
DR WPI: 1996-393336/39.
DR N-PSDB: AAT33293.
XX
PT Encapsidation of recombinant polio:virus nucleic acid for use in
PT vaccines - using a polio:virus nucleic acid which lacks the PI
PT capsid region and an expression system which provides the region
XX
PS Disclosure; Page 61-63; 108pp; English.
XX
CC cDNA sequences (AAT33293-95) respectively code for the gag, pol and
CC env proteins (AAM00179-81) of HIV-1. They can be used to substitute
CC the PI capsid gene of poliovirus in recombinant poliovirus nucleic
CC acids (rPNAs). Such rPNAs are encapsidated by introduction into
CC a host cell together with a vaccinia virus or plasmid vector
CC encoding the poliovirus PI capsid precursor protein. Encapsidated
CC rPNAs are useful for genetic immunisation, stimulating an immune
CC response to the HIV-1 protein.
XX
SQ Sequence 519 AA;
XX
Query Match 64.2%; Score 290; DB 17; Length 519;
Best Local Similarity 98.1%; Pred. No. 3.1e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHTTWLEMDREINNTYSLHSLIEESONOEKNEDELLELDKWSLMMNFI 52
DB 420 NHTTWLEMDREINNTYSLHSLIEESONOEKNEDELLELDKWSLMMNFI 471
XX
RESULT 6
AAR69997
ID AAR69997 standard; Protein; 521 AA.
XX

AC AAR69997;
XX
DT 13-SEP-1995 (first entry)
XX
DE HIV-1 env protein.
XX
KW Encapsulation; Human immunodeficiency virus; type 1; immunogenic;
XX poliovirus.
XX
OS Human immunodeficiency virus type 1.
XX
PN CA2125344-A.
XX
PD 02-JAN-1995.
XX
PF 07-JUN-1994; 94CA-2125344.
XX
PR 01-JUL-1993; 93US-0087009.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Morrow CD;
XX
DR WPI: 1995-099021/14.
DR N-PSDB; AAR69997.
XX
PT Method for encapsulating recombinant polio:virus nucleic acid -
XX useful for providing comps. to stimulate immune response.
XX
PS Disclosure; Page 38; 62pp; English.
XX
CC The sequence is that of the HIV-1 env protein. The DNA encoding
CC such protein is used in a method (claimed) to encapsulate
CC poliovirus cDNA to make it more immunogenic.
CC See also AAR69995-6.
XX
SQ Sequence 521 AA:

Query Match 64.2%; Score 290; DB 16; Length 521;
Best Local Similarity 98.1%; Pred. No. 3.1e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWMEDREINNTSLHSLSIESQNOEKNEQELLELDKWSLWMTFNI 52
ID AAR60131 standard; Protein: 856 AA.
AC AAR60131;
XX
DE 26-JUN-1991 (first entry)
XX
DE Sequence of the AIDS envelope protein.
XX
KW AIDS; HIV; LAV; HTLV-III; vaccine; antibody; epitope; antigen;
XX diagnosis.
XX
OS HTLV-III.
XX
PN EPI99301-A.
XX
PD 29-OCT-1986.
XX
PF 18-APR-1986; 86EP-0105371.
XX
PR 19-APR-1985; 85US-0725021.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (USGO) US GOVERNMENT.
PA (HEAL-) DEPT. HEALTH & HUMAN SERV.
PA (USDH) US DEPT HEALTH & HUMAN.
XX
PI Crowl RM, Gallo RC, Reddy EP, Shaw GM, Wong-Staal FY;
XX WPI: 1986-286067/44.
XX N-PSDB; AAR60128.
XX

PA (CHIR) CHIRON CORP.
XX
PI Halgwood NL, Scandella C;
XX
DR WPI: 1998-041353/04.
XX
PT Purification of HIV gp120 - using chromatographic methods
XX
PS Disclosure; Fig 2A-W; 53pp; English.
XX
XX
CC AAR60131 are fragments of the gp120 protein from different human
CC immunodeficiency virus type I (HIV-1) isolates. These proteins are used
CC in a novel method for purifying HIV gp120 so as to provide a purified
CC gp120 glycoprotein having protein/protein binding properties
CC substantially identical to natural viral HIV gp120. The method involves
CC fractionating a crude gp120 preparation containing full-length,
CC glycosylated gp120 using ion exchange chromatography so as to provide a
CC first collection of fractions. A fraction from the first collection is
CC selected that exhibits specific binding affinity for CD4 peptide,
CC thereby producing a first fractionated material. The first fractionated
CC material is fractionated by hydrophobic interaction chromatography so as
CC to provide a second collection of fractions from which a second
CC collection is selected that exhibits specific binding affinity for CD4
CC peptide. This second fraction is fractionated by size exclusion
CC chromatography so as to provide a third collection of fractions
CC exhibiting specific binding affinity for CD4 peptide, thereby providing
CC the purified gp120. The purified gp120 can be used for antibody
XX production and in vaccines.
XX
SQ Sequence 853 AA:

Query Match 64.2%; Score 290; DB 19; Length 853;
Best Local Similarity 98.1%; Pred. No. 5.4e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWMEDREINNTSLHSLSIESQNOEKNEQELLELDKWSLWMTFNI 52
ID AAR60131 standard; Protein: 856 AA.
AC AAR60131;
XX
DE 26-JUN-1991 (first entry)
XX
DE Sequence of the AIDS envelope protein.
XX
KW AIDS; HIV; LAV; HTLV-III; vaccine; antibody; epitope; antigen;
XX diagnosis.
XX
OS HTLV-III.
XX
PN EPI99301-A.
XX
PD 29-OCT-1986.
XX
PF 18-APR-1986; 86EP-0105371.
XX
PR 19-APR-1985; 85US-0725021.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (USGO) US GOVERNMENT.
PA (HEAL-) DEPT. HEALTH & HUMAN SERV.
PA (USDH) US DEPT HEALTH & HUMAN.
XX
PI Crowl RM, Gallo RC, Reddy EP, Shaw GM, Wong-Staal FY;
XX WPI: 1986-286067/44.
XX N-PSDB; AAR60128.
XX

PT Envelope protein of acquired immune deficiency syndrome virus -
PT useful for improved testing of human blood for antibodies against
PT virus and as antigen for vaccines
XX
XX Claim 33; Fig 6A; 46pp; English.
PS
CC An expression vector contg. a gene (AAN60128) coding for an envelope
CC protein of an AIDS virus, and the envelope protein of an AIDS virus
CC (AAB60131) are claimed. The vector is pref. a member of the pEV/env
CC family, e.g. pEV1.2 or 3/env 44-640 or 205-640.
XX
SQ Sequence 856 AA:

Query Match 64.2%; Score 290; DB 7; Length 856;
Best Local Similarity 98.1%; Pred. No. 5.5e-20;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWMREINNTYSLHSLTESONOEKNEOELLEDKKASIMNPNFI 52
DB 624 NHTTWMREINNTYSLHSLTESONOEKNEOELLEDKKASIMNPNFI 675

RESULT 9
AAR41025
ID AAR41025 standard; protein; 856 AA.
XX
XX AAR41025;
XX
DT 23-MAR-1994 (first entry)
XX
DE Selectively deglycosylated HIV-1 HXB2 env gp160 mutain C4.
XX
XX N-linked glycosylation; gp120; human immunodeficiency virus; type 1;
KM envelope glycoprotein; vaccine; site-directed mutagenesis.
XX
OS Human immunodeficiency virus type 1 (HXB2 strain).
XX

Key Location/Qualifiers
FT 1..30
FT /label= "signal_peptide"
FT 31..511
FT /label= "gp120"
FT /note= "exterior membrane glycoprotein"
FT 512..856
FT /label= "gp41"
FT /note= "transmembrane glycoprotein"
FT 88
FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
FT 136
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FT /note= "putative"
FT 141
FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
FT 156
FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
FT 160
FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
FT 186
FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
FT 197
FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
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FT /note= "putative"
FT 234
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FT /note= "putative"

FT Modified-site 241
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FT /note= "putative"
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FT /label= "N-linked_glycosylation_site"
FT /note= "putative"
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FT /note= "putative"
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FT /note= "putative"
FT 397
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Gln at position 386"
FT 406
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
Gln at position 397"
FT 463
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
His at position 463"
FT 463
FT /note= "putative N-linked glycosylation site
eliminated by substitution of Asn by
His at position 463"
XX W09317705-A.

PD	16-SEP-1993.	
XX		
PF	24-FEB-1993;	93WO-US01598.
XX		
PR	13-MAR-1992;	92US-0850770.
XX		
PA	(HARD)	HARVARD COLLEGE.
XX		
PI	Essex ME, Lee C, Lee T, Lee W;	
DR	WP1: 1993-303140/38.	
XX		
CC	Compsn. contg. selectively de-glycosylated HIV-1 envelope protein	
PT	- shows improved protective immune response	
XX		
PS	Clalm 7; Page 15 and 23; 45pp; English.	
XX		
CC	Mutant gp160 env protein C4 is specifically claimed. The	
CC	amino acid sequence of the muten does not appear in the	
CC	specification; sequence RA1025 has been derived from the HIV-1 HXB2	
CC	Isolate gp160 env sequence on the SWISS-Prot database (ID = ENVSHV1X,	
CC	Acc.#: P04578) and the description of C4 muten given in the	
CC	specification. The combination of changes made to N-linked	
CC	glycosylation sites in the C-terminal region of gp120 does not prevent	
CC	viral infectivity but the resultant selective deglycosylation enables	
XX	an immune response to be elicited by the muten.	
SO	Sequence 856 AA;	
	Query Match 64.2%; Score 290; DB 14; Length 856;	
	Best Local Similarity 98.1%; Pred. No. 5.5e-20;	
	Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
OY	1 NHTTWLEMDREINNTYSLIHSLIEESONQOEKNEDELDPKASIMWNT 52	
	: : : : : : : : :	
DB	624 NHTTWMDREINNTYSLIHSLIEESONQOEKNEDELDPKASIMWNT 675	
	: : : : : : : : :	
	RESULT 10	
ID	AAR41026	
XX	AAR41026 standard; protein: 856 AA.	
XX		
AC	AAR41026;	
XX		
DT	23-MAR-1994 (first entry)	
XX		
DE	Selectively deglycosylated HIV-1 HXB2 env gp160 muten C5.	
XX		
KW	N-linked glycosylation; gp120; human immunodeficiency virus; type 1;	
KW	envelope glycoprotein; vaccine; site-directed mutagenesis.	
XX		
OS	Human immunodeficiency virus type 1 (HXB2 strain).	
XX		
FH	Key	
FT	location/qualifiers	
FT	1..30	
FT	/label- signal_peptide	
FT	31..511	
FT	/label- gp120	
FT	/note- "exterior membrane glycoprotein"	
FT	512..856	
FT	/label- gp41	
FT	/note- "transmembrane glycoprotein"	
FT	88	
FT	/label- "N-linked glycosylation_site	
FT	/note- "putative"	
FT	136	
FT	/label- "N-linked glycosylation_site	
FT	/note- "putative"	
FT	141	
FT	/label- "N-linked glycosylation_site	
FT	/note- "putative"	
FT	156	
FT	/label- "N-linked glycosylation_site	

FT	Modified-site	/note- "putative"	160	/label- N-linked_glycosylation_site	/note- "putative"
FT	Modified-site	/label- N-linked_glycosylation_site	186	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	197	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	230	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	234	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	241	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	262	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	276	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	289	/note- "putative"	
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FT	Modified-site	/label- N-linked_glycosylation_site	332	/note- "putative"	
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FT	Modified-site	/label- N-linked_glycosylation_site	616	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	624	/note- "putative"	
FT	Modified-site	/label- N-linked_glycosylation_site	637	/note- "putative"	
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FT	Modified-site	/label- N-linked_glycosylation_site	750	/note- "putative"	
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FT	Modified-site	/label- N-linked_glycosylation_site	866	/note- "putative"	
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FT	/note= "exterior membrane glycoprotein"	
FT	Protein	512..856
FT	/label= gp41	
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FT	/note= "putative"	
FT	Modified-site	637
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FT	/note= "putative"	
FT	Modified-site	674

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 FT /note- "putative"
 FT Modified-site 750
 FT /label- N-linked_glycosylation_site
 FT /note- "putative"
 FT Modified-site 816
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 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 386"
 FT Misc-difference 392
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 392"
 FT Misc-difference 397
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 397"
 FT Misc-difference 406
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT Gln at position 397"
 FT Misc-difference 448
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT His at position 406"
 FT Misc-difference 463
 FT /note- "putative N-linked glycosylation site
 FT eliminated by substitution of Asn by
 FT His at position 463"
 FT W03J17705-A.
 FT 16-SEP-1993.
 FT PD
 FT 24-FEB-1993; 93WO-0501598.
 FT PR
 FT 13-MAR-1992; 92US-0850770.
 FT PA
 FT (HARD) HARVARD COLLEGE.
 FT PI
 FT Essex ME, Lee C, Lee T, Lee W;
 FT DR
 FT WPI; 1993-303140/38.
 FT XX
 FT Compns. contg. selectively de-glycosylated HIV-1 envelope protein
 FT - shows improved protective immune response
 FT PS
 FT Clalm 7; Page 15 and 23; 45pp; English.
 FT CC
 FT Mutant gp160 env protein C6 is specifically claimed. The
 FT CC amino acid sequence of the muten does not appear in the
 FT CC specification; sequence R41027 has been derived from the HIV-1 HXB2
 FT CC isolate gp160 env sequence on the SWISS-PROT database (ID = ENVSHV1X,
 FT CC Acc.#: P04578) and the description of C6 muten given in the
 FT CC specification. The combination of changes made to N-linked
 FT CC glycosylation sites in the C-terminal region of gp120 does not prevent
 FT CC viral infectivity but the resultant selective deglycosylation enables
 FT CC an immune response to be elicited by the muten.
 FT CC
 FT XX
 FT Sequence 856 AA;
 FT
 FT Query Match 64.2%; Score 290; DB 14; Length 856;
 FT Best Local Similarity 98.1%; Pred. No. 5.5e-20;
 FT Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
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 ID AAR41028 standard; protein; 856 AA.
 XX
 AC AAR41028;
 XX
 DT 23-MAR-1994 (first entry)
 XX
 DE Selectively deglycosylated HIV-1 HXB2 env gp160 muten Q.
 XX
 DE N-linked glycosylation; gp120; human immunodeficiency virus; type 1;
 KW envelope glycoprotein; vaccine; site-directed mutagenesis.
 XX
 OS Human immunodeficiency virus type 1 (HXB2 strain).
 XX
 FH Key
 FT Peptide
 FT Protein
 FT Protein
 FT
 FT Location/Qualifiers
 FT 1..30
 FT /label- signal_peptide
 FT 31..511
 FT /label- gp120
 FT /note- "exterior membrane glycoprotein"
 FT 512..856
 FT /label- gp41
 FT /note- "transmembrane glycoprotein"
 FT 88
 FT /label- N-linked_glycosylation_site
 FT /note- "putative"
 FT 136
 FT /label- N-linked_glycosylation_site
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XX	24-FEB-1993;	93WO-US01598.
PF		
XX	13-MAR-1992;	92US-0850770.
XX		
XX	(HARD) HARVARD COLLEGE.	
PA		
XX	Essex ME, Lee C, Lee T, Lee W;	
PI		
XX	WPI; 1993-303140/38.	
DR		
XX		
PT	Compsn. contg. selectively de-glycosylated HIV-1 envelope protein	
PT	- shows improved protective immune response	
XX		
PS	Claim 7; Page 18, 23 and 26; 45pp; English.	
XX		
CC	Mutant gp160 env protein R is specifically claimed. The	
CC	amino acid sequence of the muten does not appear in the	
CC	specification; sequence R41029 has been derived from the HIV-1 HXB2	
CC	isolate gp160 env sequence on the SWISS-PROT database (ID = ENVSHIV1X,	
CC	Acc. #: P04578) and the description of R muten given in the	
CC	specification. The combination of changes made to N-linked	
CC	glycosylation sites in the C-terminal region of gp120 does not prevent	
CC	viral infectivity but the resultant selective deglycosylation enables	
CC	an immune response to be elicited by the muten.	
XX		
SQ	Sequence 856 AA;	
	Query Match 64.2%; Score 290; DB 14; Length 856;	
	Best Local Similarity 98.1%; Pred. No. 5.5e-20;	
	Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0.	
OY	1 NHTTWLEMDREINNTSLIHSLEIESONQOEKNEQELLELDKWSIMWNFI 52	
	: : : : : : : : :	
DB	624 NHTTWLEMDREINNTSLIHSLEIESONQOEKNEQELLELDKWSIMWNFI 675	
	: : : : : : : : :	
RESULT 14		
ID	AAR41030 standard; protein; 856 AA.	
XX		
AC	AAR41030;	
XX		
DT	23-MAR-1994 (first entry)	
XX		
DE	Selectively deglycosylated HIV-1 HXB2 env gp160 muten S.	
KW	N-linked glycosylation; gp120; human immunodeficiency virus; type 1;	
KW	envelope glycoprotein; vaccine; site-directed mutagenesis.	
XX		
OS	Human immunodeficiency virus type 1 (HXB2 strain).	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..30
FT		/label- signal_peptide
FT	Protein	31..511
FT		/label- gp120
FT		/note- "exterior membrane glycoprotein"
FT	Protein	512..856
FT		/label- gp41
FT		/note- "transmembrane glycoprotein"
FT	Modified-site	88
FT		/label- N-linked_glycosylation_site
FT		/note- "putative"
FT	Modified-site	136
FT		/label- N-linked_glycosylation_site
FT		/note- "putative"
FT	Modified-site	141
FT		/label- N-linked_glycosylation_site
FT		/note- "putative"
FT	Modified-site	156
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FT		/note- "putative"

FT	Modified-site	160	/label- N-linked glycosylation_site
FT		/note-	"putative"
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FT		/note-	"putative"
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FT		/note-	"putative"
FT	Modified-site	816	/label- N-linked glycosylation_site
FT		/note-	"putative"
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FT	Misc-difference	339	"putative N-linked glycosylation site eliminated by substitution of Asn by His at position 332"
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FT	Misc-difference	386	"putative N-linked glycosylation site eliminated by substitution of Asn by Gln at position 339"

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 FT /note= "exterior membrane glycoprotein"
 FT 512..856
 FT /label= gp41
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 FT 463
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 FT /note= "putative N-linked glycosylation site eliminated by substitution of Asn by His at position 463"
 FT W09317705-A.
 FT 16-SEP-1993.
 FT PD
 FT XX 24-FEB-1993; 93WO-US01598.
 FT PF
 FT XX 13-MAR-1992; 92US-0850770.
 FT PR
 FT XX (HARD) HARVARD COLLEGE.
 FT PA
 FT PI Essex ME, Lee C, Lee T, Lee W;
 FT DR WPI, 1993-303140/38.
 FT XX
 FT PT Compn. contg. selectively de-glycosylated HIV-1 envelope protein
 FT PT - shows improved protective immune response
 FT XX
 FT PS Claim 7; Page 18, 23 and 26; 45pp: English.
 FT XX
 FT CC Mutant gp160 env protein T is specifically claimed. The
 FT CC amino acid sequence of the mutlein does not appear in the
 FT CC specification; sequence R41031 has been derived from the HIV-1 HXB2
 FT CC isolate gp160 env sequence on the SWISS-PROT database (ID = ENVSHV1X,
 FT CC Acc.#: P04578) and the description of T mutlein given in the
 FT CC specification. The combination of changes made to N-linked
 FT CC glycosylation sites in the C-terminal region of gp120 does not prevent
 FT CC viral infectivity but the resultant selective deglycosylation enables
 FT CC an immune response to be elicited by the mutlein.
 FT CC
 FT XX
 FT SQ Sequence 856 AA:
 FT
 FT Query Match 64.2%; Score 290; DB 14; Length 856;
 FT Best Local Similarity 98.1%; Pred. No. 5.5e-20;
 FT Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 FT
 FT Oy 1 NHTTWLEMDREINNTSLHSLSIESQNOQRKEGELLEDRKSLAWMPFI 52
 FT Db 624 NHTTWLEMDREINNTSLHSLSIESQNOQRKEGELLEDRKSLAWMPFI 675

Wed May 7 14:34:27 2003

us-09-877-606-4.rag

Page 13

Search completed: May 7, 2003, 09:53:52
Job time : 77.5231 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 28.7269 Seconds
(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-4

Perfect score: 452
Sequence: 1 NHTTWLEMDREINNTYSLIH.....SKIYHIEINRIKILIGER 85

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	61.3	851	2	env polypeptin -
2	277	61.3	854	2	env polypeptin - huma
3	277	61.3	856	1	env polypeptin pr
4	277	61.3	861	1	env polypeptin pr
5	268	59.3	856	1	env polypeptin pr
6	261	57.7	858	1	env polypeptin pr
7	254	56.2	856	1	env polypeptin pr
8	253	56.0	861	1	env polypeptin pr
9	251	55.5	443	2	env polypeptin p
10	247	54.6	847	2	env polypeptin p
11	247	54.6	847	2	env polypeptin p
12	246	54.4	852	2	env polypeptin - huma
13	245	54.2	357	2	env polypeptin - huma
14	244	54.0	358	2	env polypeptin g
15	244	54.0	358	2	env polypeptin g
16	244	54.0	358	2	env polypeptin g
17	243	53.8	859	1	env polypeptin g
18	242	53.5	357	2	env polypeptin pr
19	241	53.3	357	2	env polypeptin pr
20	241	53.3	853	2	env polypeptin g
21	241	53.3	855	1	env polypeptin g
22	240	53.1	357	2	env polypeptin pr
23	239	52.9	852	1	env polypeptin g
24	237	52.4	357	2	env polypeptin -
25	237	52.4	445	2	env polypeptin M
26	236	52.2	729	1	env polypeptin pr
27	236	52.2	855	1	env polypeptin pr
28	236	52.2	861	1	env polypeptin pr
29	236	52.2	868	1	env polypeptin -

30	234	51.8	846	1	VCLJND	env polypeptin pr
31	233	51.5	843	1	H44001	env polypeptin pr
32	230	50.9	859	2	T01672	env polypeptin pr
33	228	50.4	136	2	JU0266	env polypeptin pr
34	228	50.4	454	2	B41621	env polypeptin D
35	223	49.3	136	2	UT0954	env polypeptin pr
36	215	47.6	856	1	A44963	env polypeptin pr
37	213	47.1	357	2	S21990	env polypeptin g
38	198	43.8	854	2	VCLJST	env polypeptin pr
39	197	43.6	877	2	S49197	env polypeptin pr
40	181	40.0	863	2	A53034	env polypeptin p
41	137.5	30.4	881	1	VCLJG3	gag polypeptin -
42	136	30.1	281	1	RG87A2	env polypeptin -
43	133.5	29.5	151	2	S30448	amino acid biosynt
44	133.5	29.5	151	2	S30452	env polypeptin - huma
45	133.5	29.5	881	2	S03068	env polypeptin - huma

ALIGNMENTS

RESULT 1

env polypeptin - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_rev19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlnt, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:211530; NID:960192; PIDN:CAAT7628.1; PID:960199

C:Superfamily: type E retrovirus env polypeptin

Query Match

Best local Similarity 61.3%; Score 277; DB 2; Length 851;

Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query 1 NHTTWLEMDREINNTYSLIHESONOEKNEDELLEDKWASLMMWNI 52

DB 619 NHTTWLEMDREINNTYSLIHESONOEKNEDELLEDKWASLMMWNI 670

RESULT 2

env polypeptin - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_rev19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Tiller, K.; Zack, Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MVID:91043044; PMID:2172833

A:Accession: S13288

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptin

Query Match

Best local Similarity 61.3%; Score 277; DB 2; Length 854;

Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query 1 NHTTWLEMDREINNTYSLIHESONOEKNEDELLEDKWASLMMWNI 52

DB 622 NHTTWLEMDREINNTYSLIHESONOEKNEDELLEDKWASLMMWNI 673

RESULT 3

VCLJH3

env polypeptin -

env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Lyak, K.J.; Starcich, B.; Josephs, S.F.; Dora-
mberger, J.A.; Papas, T.S.; Ghayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 61.3%; Score 277; DB 1; Length 856;
Best Local Similarity 94.2%; Pred. No. 4.4e-16;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 52
DB 624 NMTWMEWDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 675

RESULT 4

VCLJVL

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allzon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:85099333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <MAT>
A:Cross-references: GB:K02013; NID:9326417; PIDN:AB59751.1; PID:9326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 61.3%; Score 277; DB 1; Length 861;
Best Local Similarity 94.2%; Pred. No. 4.5e-16;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 52
DB 629 NMTWMEWDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 680

RESULT 5

VCLJVL

env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polyprotein

C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Musning, M.A.; Smith, D.H.; Cabridilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93355; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUD>
A:Cross-references: GB:K02083; NID:9555008; PIDN:AB59873.1; PID:9328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre
Query Match 59.3%; Score 268; DB 1; Length 856;
Best Local Similarity 90.4%; Pred. No. 2.6e-15;
Matches 47; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 52
DB 624 NMTWMEWDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 675

RESULT 6

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
Submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STEL>
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STEZ>
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183
C:Superfamily: type E retrovirus env polyprotein

Query Match 57.7%; Score 261; DB 2; Length 358;
Best Local Similarity 60.0%; Pred. No. 3.8e-15;
Matches 51; Conservative 11; Mismatches 11; Indels 12; Gaps 1;

OY 1 NHTTWLEMDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 60
DB 126 NMTWMEWDREINNTSLIHSLEESQNOEKNEDELLELDKMSLWMMFNI 175

OY 61 IEELISKYHENEIARIKKLIGER 85
DB 176 --DITQWLMYIKIFIMYGLIGLR 198

RESULT 7

VCLJ3W

env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)

N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: GB:K03455; GB:M38432; MID:g1906382
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-841/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 56.2%; Score 254; DB 1; Length 856;
Best Local Similarity 84.6%; Pred. No. 4,1e-14;
Matches 44; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NHTWLEMDREINNTYSLIHSLEESQNOEKNEQELLEDKWSLWNNFNI 52
Db 624 NNTWMEWEIEDNTSLIYTLIEESQNOEKNEQELLEDKWSLWNNFNI 675

RESULT 8

VCLJSC
env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sci
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polypeptide #status predicted <EP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 56.0%; Score 253; DB 1; Length 861;
Best Local Similarity 89.8%; Pred. No. 5e-14;
Matches 44; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TWLEMDREINNTYSLIHSLEESQNOEKNEQELLEDKWSLWNNFNI 52
Db 632 TWMEWEIEDNTSLIYTLIEESQNOEKNEQELLEDKWSLWNNFNI 680

RESULT 9

CA1621
env polypeptide P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat polypeptide
C:Species: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C:Accession: CA1621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversi
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: CA1621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: GB:M77230; MID:g328631; PIDN:AA803792.1; PID:9555015
A:Note: This virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TMN>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:

Query Match 55.5%; Score 251; DB 2; Length 443;
Best Local Similarity 57.6%; Pred. No. 3.5e-14;
Matches 49; Conservative 13; Mismatches 11; Indels 12; Gaps 1;

Qy 1 NHTWLEMDREINNTYSLIHSLEESQNOEKNEQELLEDKWSLWNNFNI 60
Db 364 NNTWMEWEIEDNTSLIYTLIEESQNOEKNEQELLEDKWSLWNNFNI 414

Qy 61 IEELISIKYIHEINELARKLIGER 85
Db 415 ---ITNMLWYIKFIIVGLIGLR 436

RESULT 10

T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JREFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akash, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz
submitted to the EMBL Data Library, July 1996
A:Reference number: T09448
A:Accession: T09448
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: EMBL:U03632; MID:g1465777; PID:g1465781
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide

Query Match 54.6%; Score 247; DB 2; Length 847;
Best Local Similarity 82.7%; Pred. No. 1.6e-13;
Matches 43; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

Qy 1 NHTWLEMDREINNTYSLIHSLEESQNOEKNEQELLEDKWSLWNNFNI 52
Db 615 NNTWMEWEIEDNTSLIYTLIEESQNOEKNEQELLEDKWSLWNNFNI 666

RESULT 11

S13289
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13289
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack,
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1
A:Reference number: S13289; MUID:91043044; PMID:2172833
A:Accession: S13289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OBR>
C:Superfamily: type E retrovirus env polypeptide

Query Match 54.6%; Score 247; DB 2; Length 847;

Best Local Similarity 82.7%; Pred. No. 1.6e-13;
Matches 43: Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEOELLELDKWSLWNNFNI 52
Db 615 NMTWMEWREIDNTSLIYTLIESONQOEKNEOELLELDKWSLWNNFNI 666

RESULT 12

712016

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T12016

R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.

AIDS Res. Hum. Retroviruses 14, 329-337, 1998

A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S

A:Reference number: 217379; MUID:9818716; PMID:9519894

A:Accession: T12016

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-852 <MC>

A:Cross-references: EMBL:U09034; NID:q2351783; PIDN:ACG59271.1; PID:q2351784

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match 54.4%; Score 246; DB 2; Length 852;

Best Local Similarity 57.6%; Pred. No. 2e-13;

Matches 49: Conservative 12; Mismatches 12; Indels 12; Gaps 1;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEOELLELDKWSLWNNFNI 60
Db 620 NMTWMEWREIDNTSLIYTLIESONQOEKNEOELLELDKWSLWNNFNI 669

OY 61 IEELISKIYHENEIARIKILIGER 85
Db 670 --DITKMLYIKIFIMVGLIGLR 692

RESULT 13
S21996

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S70422; S21996

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cereb

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70422

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61356; NID:q60181; PIDN:CAA43624.1; PID:q1067129

A:Experimental source: patient 27L

A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 54.2%; Score 245; DB 2; Length 357;

Best Local Similarity 56.5%; Pred. No. 8.9e-14;

Matches 48: Conservative 13; Mismatches 12; Indels 12; Gaps 1;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEOELLELDKWSLWNNFNI 60
Db 125 DNMTWMEWREIDNTSLIYTLIESONQOEKNEOELLELDKWSLWNNFNI 175

OY 61 IEELISKIYHENEIARIKILIGER 85
Db 176 --ITNMLYIKIFIMVGLIGLR 197

RESULT 14

S22002

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Vary: isolate 3L

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S22002; S70418

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22002

A:Molecule type: DNA

A:Residues: 1-358 <ST2>

A:Cross-references: EMBL:X61352; NID:q60186; PIDN:CAA43616.1; PID:q60187

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333, 'X', 335-358 <ST2>

A:Cross-references: EMBL:X61352; NID:q60186

C:Superfamily: type E retrovirus env polyprotein

Query Match 54.0%; Score 244; DB 2; Length 358;

Best Local Similarity 80.8%; Pred. No. 1.1e-13;

Matches 42: Conservative 8; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEOELLELDKWSLWNNFNI 52
Db 126 DNMTWMEWREIDNTSLIYTLIESONQOEKNEOELLELDKWSLWNNFNI 177

RESULT 15
S22000

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995

C:Accession: S22000

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete

A:Reference number: S21990

A:Accession: S22000

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <ST2>

A:Cross-references: EMBL:X61351

C:Superfamily: type E retrovirus env polyprotein

Query Match 54.0%; Score 244; DB 2; Length 358;

Best Local Similarity 80.8%; Pred. No. 1.1e-13;

Matches 42: Conservative 8; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEOELLELDKWSLWNNFNI 52
Db 126 DNMTWMEWREIDNTSLIYTLIESONQOEKNEOELLELDKWSLWNNFNI 177

Search completed: May 7, 2003, 09:58:38

Job time: 29.7269 secs


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FT DISULFD 385 418 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97212 MM; 6FAB16AF85107FED0 CRC64;

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Query Match 64.2%; Score 290; DB 1; Length 856;
Best Local Similarity 98.1%; Pred. No. 3.7e-18;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NHTTWLEMDREINNTSLIHSIESQNOQEKNEQELLEDKWASLWMMFNI 52
DB 624 NHTTWLEMDREINNTSLIHSIESQNOQEKNEQELLEDKWASLWMMFNI 675

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RESULT 2

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ENV_HV1H3 STANDARD; PRT; 856 AA.
AC P04624;

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DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
CX NCBI_TaxID=11707;

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RA MEDLINE=85228248; PubMed=2988795;

```

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RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R.,
Shaw G.M., Wong-Staal F., Reddy E.P.;

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RT "HIV-1: env gene products synthesized in E. coli are recognized by
antibodies present in the sera of AIDS patients."

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RL Cell 41:979-986(1985).

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entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).

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DR EMBL; M14100; AAA44679.1; -
DR HIV; M14100; ENVSHXB3.
DR InterPro; IPR000328; ENV_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120.1.
DR Pfam; PF00517; GP41.1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
Signal.

```

```

FT SIGNAL 1 30
FT CHAIN 512 856
FT DISULFD 119 205
FT DISULFD 126 196
FT DISULFD 131 157
FT DISULFD 218 247
FT DISULFD 228 239
FT DISULFD 296 331
FT DISULFD 378 445
FT DISULFD 385 418

```

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FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MM; 337368BB84C1AFC CRC64;

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Query Match 64.2%; Score 290; DB 1; Length 856;
Best Local Similarity 98.1%; Pred. No. 3.7e-18;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NHTTWLEMDREINNTSLIHSIESQNOQEKNEQELLEDKWASLWMMFNI 52
DB 624 NHTTWLEMDREINNTSLIHSIESQNOQEKNEQELLEDKWASLWMMFNI 675

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RESULT 3

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ENV_HV1LM STANDARD; PRT; 856 AA.
AC Q70626;

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DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.

```

OX NCBI_TaxID=82834;
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE-95127297; PubMed-7826699;
 RA Reitz M.S. Jr., Hall L., Robert-Groff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type 111B).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 CC
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 CC
 CC EMBL: U12055; AAA76690.1; -
 DR Glycosylated; Q70626; -
 DR InterPro: IPR000328; Env-CP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL.
 FT CHAIN
 FT 1 30
 FT 511 511
 FT 512 856
 FT 54 74
 FT 119 205
 FT 126 196
 FT 131 157
 FT 218 247
 FT 228 239
 FT 296 331
 FT 378 445
 FT 385 418
 FT 88 88
 FT 136 136
 FT 141 141
 FT 156 156
 FT 160 160
 FT 186 186
 FT 197 197
 FT 230 230
 FT 234 234
 FT 241 241
 FT 262 262
 FT 276 276
 FT 289 289
 FT 295 295
 FT 301 301
 FT 332 332
 FT 339 339
 FT 356 356
 FT 386 386
 FT 392 392
 FT 397 397
 FT 406 406
 FT 448 448
 FT 463 463
 FT 611 611
 FT 616 616
 FT 624 624
 FT 637 637
 FT 674 674
 FT 750 750
 FT 816 816
 FT 856 AA;
 SQ SEQUENCE
 64.2%; Score 290; DB 1; Length 856;
 Best Local Similarity 98.1%; Pred. No. 3.7e-18;

Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NHTTWLEMDREINNTYSLHSLEESQNOEKNEQELDKWASIMNNFNI 52
 Db 624 NHTTWLEMDREINNTYSLHSLEESQNOEKNEQELDKWASIMNNFNI 675
 RESULT 4
 ID ENV_HV1B8 STANDARD; PRT: 851 AA.
 AC P04582;
 DT 13-AUG-1987 (rel. 05; Created)
 DT 13-AUG-1987 (rel. 05; Last sequence update)
 DT 15-JUL-1999 (rel. 38; Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11684;
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE-85111123; PubMed-2578615;
 RA Ratner L., Haseltine W., Patarca R., Lyvak K.J., Starcich B.R.,
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
 RA Baumeister K., Ivanoff L., Petway S.R. Jr., Pearson M.L.,
 RA Lautenberger J.A., Paps T.S., Grayeb J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RT Nature 313:277-284(1985).
 RL
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 CC or send an email to license@sdb-sdb.ch).
 CC
 CC EMBL: K02011; AAA44661.1; -
 DR HIV: K02011; ENVS8B8.
 DR Glycosylated; P04582; -
 DR InterPro: IPR000328; Env-CP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL.
 FT CHAIN
 FT 1 30
 FT 507 506
 FT 512 851
 FT 54 74
 FT 119 205
 FT 126 196
 FT 131 157
 FT 218 247
 FT 228 239
 FT 296 331
 FT 378 440
 FT 385 413
 FT 88 88
 FT 136 136
 FT 141 141
 FT 156 156
 FT 160 160
 FT 186 186
 FT 197 197
 FT 230 230
 FT 234 234
 FT 241 241
 FT 262 262
 FT 276 276
 FT 295 295
 SQ SEQUENCE
 64.2%; Score 290; DB 1; Length 856;
 Best Local Similarity 98.1%; Pred. No. 3.7e-18;

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; D16A3C90857785F1 CRC64;

Query Match 61.3%; Score 277; DB 1; Length 851;
 Best Local Similarity 94.2%; Pred. No. 5e-17;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTWLEMDREINNTSLHSIESONQOEKNEOLLELDKASLWNNFNI 52
 DB 619 NNMWMDREINNTSLHSIESONQOEKNEOLLELDKASLWNNFNI 670
 1:|||||

RESULT 5
 ENV_HV1B1 STANDARD; PRT; 856 AA.
 AC P03375;
 ID ENV_HV1B1
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 CC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Lyvak K.J., Starcich B.R.,
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
 RA Baumesler K., Ivanoff L., Pelleway S.R., Jr., Pearson M.L.,
 RA Latenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284(1985).
 RN [2]
 RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=90285159; PubMed=2355006;
 RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
 RA Gregory T.J.;
 RT "Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type 1 recombinant human immunodeficiency virus envelope glycoprotein (gp120) expressed in Chinese hamster ovary cells.";
 RL J. Biol. Chem. 265:10373-10382(1990).
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 CC EMBL, M15654, AAA44205.1; -;
 DR PIR: A03973; VCLJH3.
 DR HIV: M15654; ENV5BH102.
 DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 625 625
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97224 MW; 0BFPIA18931B27 CRC64;

Query Match 61.3%; Score 277; DB 1; Length 856;
 Best Local Similarity 94.2%; Pred. No. 5e-17;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTWLEMDREINNTSLHSIESONQOEKNEOLLELDKASLWNNFNI 52
 DB 624 NNMWMDREINNTSLHSIESONQOEKNEOLLELDKASLWNNFNI 675
 1:|||||

RESULT 6
 ENV_HV1B1 STANDARD; PRT; 861 AA.
 AC P03377;
 ID ENV_HV1B1
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 CC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11678;
 RN [1]

FT CARBOHD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 614 614 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 623 623 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 672 672 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 748 748 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 814 814 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96912 MW; 337B93B6F22ABA CRC64;

Query Match 60.6%; Score 274; DB 1; Length 853;
 Best Local Similarity 92.3%; Pred. No. 9.2e-17;
 Matches 48; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 NHTTWLEMDREINNTSLHSIESONQOEKNEDELLEDKWASLWMTNI 52
 Db 622 NMTWMDREINNTSLHSIESONQOEKNEDELLEDKWASLWMTNI 673

ENV_HV1PV STANDARD; PRT; 856 AA.
 ID ENV_HV1PV
 AC P03376;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=8511157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;
 RT "Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
 CC -----
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 CC -----
 CC EMBL: K02083; AAB59873.1; -;
 DR EMBL: X01762; CAA25903.1; ALT_SEQ.
 DR PIR: A03974; VCLJVL.
 DR HIV: K02083; ENVSPV22.
 DR InterPro: IPR000328; Env-GP41.
 DR Pfam: PF00516; GP120.1.
 DR Pfam: PF00517; GP41.1.
 DR AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 KW SIGNAL.
 FT CHAIN 1 30
 FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT DISULFD 512 856 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFD 54 74
 FT DISULFD 119 205 BY SIMILARITY.
 FT DISULFD 126 196 BY SIMILARITY.
 FT DISULFD 131 157 BY SIMILARITY.
 FT DISULFD 218 247 BY SIMILARITY.
 FT DISULFD 228 239 BY SIMILARITY.

FT DISULFD 296 331 BY SIMILARITY.
 FT DISULFD 378 445 BY SIMILARITY.
 FT DISULFD 385 418 BY SIMILARITY.
 FT CARBOHD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97339 MW; 5FCDB1DC3C120983 CRC64;

Query Match 59.3%; Score 268; DB 1; Length 856;
 Best Local Similarity 90.4%; Pred. No. 3.1e-16;
 Matches 47; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 1 NHTTWLEMDREINNTSLHSIESONQOEKNEDELLEDKWASLWMTNI 52
 Db 624 NMTWMDREINNTSLHSIESONQOEKNEDELLEDKWASLWMTNI 675

ENV_HV1W1 STANDARD; PRT; 856 AA.
 ID ENV_HV1W1
 AC P31872;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=31678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86218077; PubMed=2423250;
 RA Starck B.S., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Joseph S.F., Gallo R.C., Wong-Staal F.;
 RT "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";
 RL Cell 45:637-648(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
 CC PIR: A24774; VCLJ3W.
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.

-1- MISPLANNED: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
1984 IN SOUTHERN CALIFORNIA.

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CC CC
DR EMBL; M17450; -; NOT_ANNOTATED_CDS.
DR HIV; B28932; VCLJSC.
DR HIV; M17450; ENVSSC.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
Signal.
KW Signal.
FT SIGNAL 1 29
FT CHAIN 510 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.
FT SITE 760 760 IN-FRAME TERMINATION CODON.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 160 BY SIMILARITY.
FT DISULFID 219 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 330 BY SIMILARITY.
FT DISULFID 376 439 BY SIMILARITY.
FT DISULFID 383 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC . .) (POTENTIAL).
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FT CARBOHYD 331 331 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 354 354 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 360 360 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 384 384 N-LINKED (GLCNAC . .) (POTENTIAL).
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FT CARBOHYD 405 405 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 625 625 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;

Query Match 56.0%; Score 253; DB 1; Length 856;
Best Local Similarity 89.8%; Pred. No. 6.3e-15;
Matches 44; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

4 TWLEMDREINNVTSLHLSIEESQNOQERKDELLDKWASLAWMFI 52

[illegible]

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FT FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 847 AA; 96135 MW; 04901317ED7FE2AB CRC64;

Query Match 55.8%; Score 252; DB 1; Length 847;
Best Local Similarity 58.1%; Pred. No. 7.7e-15;
Matches 50; Conservative 14; Mismatches 8; Indels 14; Gaps 2.

OY 1 NHTTLEMDREINNTYSLIHSLSIESQNOKEKEOELLEDKWASLWMFNIRIKOIEDK 60
Dd 615 NNMWMEWEREDNTNLTLYTLESQNOKEKEOELLEDKWASLWMFNFI----- 666
OY 61 IEELISK-LYHTENELARIKKLIGER 85
Dd 667 -----SKWLMTYKIRITMTVGLVGLR 687

RESULT 12
ENV_HV1S3 STANDARD: PRT: 852 AA.
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentiviridae.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D, Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range,
replication, and cytopathicity are linked to the envelope region of
the viral genome.";
RL J. Virol. 64:4016-4020(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR DR EMBL: M38427; AAAA5067.1; -.
DR DR HIV; M38427; ENVSEP33.
DR DR InterPro; IPR000328; Env_GP41.
DR DR InterPro; IPR000777; GP120.
DR DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW signal.
FT FT SIGNAL 1 31
FT FT CHAIN 32 506 BY SIMILARITY.
FT FT CHAIN 507 852 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
FT FT DISULFID 118 206 BY SIMILARITY.
FT FT DISULFID 125 197 BY SIMILARITY.
FT FT DISULFID 130 156 BY SIMILARITY.
FT FT DISULFID 219 248 BY SIMILARITY.
FT FT DISULFID 229 240 BY SIMILARITY.
FT FT DISULFID 297 331 BY SIMILARITY.
FT FT DISULFID 377 439 BY SIMILARITY.
FT FT DISULFID 384 412 BY SIMILARITY.
FT FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 852 AA; 96663 MW; E7BFB0D23C9910D CRC64;

Query Match 52.8%; Score 252; DB 1; Length 852;
Best Local Similarity 82.7%; Pred. No. 7.7e-15;
Matches 43; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLHSLEESONOEKNEDELLEDKWASLMMWFNI 52
Db 620 NNTTWMEWEEDINTSYLSLYLLEESONOEKNEDELLEDKWASLMMWFSI 671

RESULT 13
ENV_HY1W2 STANDARD; PRT; 847 AA.
ID ENV_HY1W2
AC P05880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=6635450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salubuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HIV-1/HIV/LAV over time in patients with AIDS or at risk for AIDS."
RL Science 233:1548-1553(1986).
CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
CC
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CC
CC EMBL: M12507; AAB12990.1; -
CC DR HIV; M12507; ENVSWMJ2.
CC DR InterPro: IPR000328; Env GP41.
CC DR InterPro: IPR000777; GP120.

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DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 29
FT CHAIN 30 501
FT CHAIN 502 847
FT DISULFID 53 73
FT DISULFID 118 202
FT DISULFID 125 193
FT DISULFID 130 152
FT DISULFID 215 244
FT DISULFID 225 236
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FT CARBOHYD 87 87
FT CARBOHYD 134 134
FT CARBOHYD 140 140
FT CARBOHYD 151 151
FT CARBOHYD 155 155
FT CARBOHYD 183 183
FT CARBOHYD 184 184
FT CARBOHYD 194 194
FT CARBOHYD 231 231
FT CARBOHYD 238 238
FT CARBOHYD 259 259
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FT CARBOHYD 286 286
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FT CARBOHYD 386 386
FT CARBOHYD 390 390
FT CARBOHYD 400 400
FT CARBOHYD 438 438
FT CARBOHYD 450 450
FT CARBOHYD 602 602
FT CARBOHYD 607 607
FT CARBOHYD 616 616
FT CARBOHYD 628 628
SQ SEQUENCE 847 AA; 96466 MW; CD1E33D73AA5BCAE CRC64;

Query Match 54.2%; Score 245; DB 1; Length 847;
Best Local Similarity 56.5%; Pred. No. 3.1e-14;
Matches 48; Conservative 14; Mismatches 11; Indels 12; Gaps 1;

QY 1 NHTTWLEMDREINNTSLHSLEESONOEKNEDELLEDKWASLMMWFNIKIQEDK 60
Db 615 DNTTWMEWEEDINTSYLSLYLLEESONOEKNEDELLEDKWASLMMWFNIKIQEDK 664
QY 61 IEEILSKYHIENEIARIKIKIGER 85
Db 665 -DITWMLWIKIFIMVGLIGIR 687

RESULT 14
ENV_HY1W2 STANDARD; PRT; 856 AA.
ID ENV_HY1W2
AC P05877;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 60.9954 Seconds
(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-4

Perfect score: 452
Sequence: 1 NHTTWLEWDEIRNNTSLIR.....SKYHIENIARIKKLIGER 85

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP:archaea:21:1
2: SP:bacteria:1
3: SP:fungi:1
4: SP:human:1
5: SP:invertebrate:1
6: SP:mammal:1
7: SP:mhc:1
8: SP:organelle:1
9: SP:phage:1
10: SP:plant:1
11: SP:rodent:1
12: SP:virus:1
13: SP:vertebrate:1
14: SP:unclassified:1
15: SP:viirus:1
16: SP:bacteriap:1
17: SP:archaeap:1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	64.2	748	15	Q70606 human immun
2	290	64.2	752	15	Q70604 human immun
3	290	64.2	752	15	Q70605 human immun
4	286	63.3	747	15	Q70607 human immun
5	286	63.3	752	15	Q70608 human immun
6	285	63.1	856	15	Q90SM7 human immun
7	282	62.4	852	15	Q89797 human immun
8	280	61.9	856	15	Q92877 human immun
9	277	61.3	645	15	Q99346 human immun
10	277	61.3	851	15	Q78243 human immun
11	277	61.3	851	15	Q85582 human immun
12	277	61.3	854	15	Q72502 human immun
13	277	61.3	856	15	Q74599 human immun
14	277	61.3	856	15	Q74090 human immun
15	273	60.4	854	15	Q90178 human immun
16	273	60.4	854	15	Q78705 human immun

17	270	59.7	757	15	Q9Q722 human immun
18	265	58.6	851	15	Q56110 human immun
19	265	58.6	855	15	Q9E1R7 human immun
20	264	58.4	848	15	Q69990 human immun
21	262	58.0	727	15	Q9Q723 human immun
22	261	57.7	358	15	Q78120 human immun
23	261	57.7	616	15	Q993B0 human immun
24	261	57.7	618	15	Q993B2 human immun
25	261	57.7	854	15	Q78225 human immun
26	260	57.5	838	15	Q03806 human immun
27	260	57.5	848	15	Q69988 human immun
28	260	57.5	855	15	Q03805 human immun
29	260	57.5	862	15	Q9E1S2 human immun
30	259	57.3	635	15	Q90U82 human immun
31	259	57.3	856	15	Q69992 human immun
32	257	56.9	856	15	Q72993 human immun
33	257	56.9	859	15	Q8Q863 human immun
34	257	56.9	863	15	Q9WU04 human immun
35	257	56.9	864	15	Q9YU48 human immun
36	256	56.6	851	15	Q8Q852 human immun
37	256	56.6	854	15	Q56112 human immun
38	256	56.6	863	15	Q9WU08 human immun
39	256	56.6	863	15	Q42031 human immun
40	256	56.6	864	15	Q9WU01 human immun
41	255	56.4	847	15	Q69996 human immun
42	255	56.4	849	15	Q71974 human immun
43	254	56.2	849	15	Q77368 human immun
44	254	56.2	858	15	Q8Q867 human immun
45	254	56.2	858	15	Q8Q865 human immun

ALIGNMENTS

RESULT 1
ID Q70606 PRELIMINARY; PRT: 748 AA.
AC Q70606;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RX MEDLINE-95127297; PubMed-7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B., Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W., "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type 111B)."
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RL [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12032; AAA76668.1;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP41.1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER
SQ SEQUENCE 748 AA; 84224 MW; 56BDEF186C67694B CRC64;

Query Match 64.2%; Score 290; DB 15; Length 748;
Best Local Similarity 98.1%; Pred. No. 4.3e-16;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 52
DB 620 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 671

RESULT 2
OY 070604 PRELIMINARY: PRT: 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-LW851;
RA Mulder K.E.;
RA Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; U12030; AAA7666.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 64.2%; Score 290; DB 15; Length 752;
Best Local Similarity 98.1%; Pred. No. 4.5e-16;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 52
DB 624 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 675

RESULT 3
OY 070605 PRELIMINARY: PRT: 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW852;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-LW852;
```

```
RA Mulder K.E.;
RL Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; U12031; AAA7666.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 64.2%; Score 290; DB 15; Length 752;
Best Local Similarity 98.1%; Pred. No. 4.5e-16;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 52
DB 624 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 675

RESULT 4
OY 070607 PRELIMINARY: PRT: 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HTLV type IIIB).";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-LW87-1;
RA Mulder K.E.;
RA Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL; U12034; AAA7666.1; -.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732EB836A522A5F14 CRC64;

Query Match 63.3%; Score 286; DB 15; Length 747;
Best Local Similarity 98.1%; Pred. No. 9.5e-16;
Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 52
DB 619 NHTTWLEMDREINNTSLIHSIESONQOEKNEQELLELDKWSLWMWNT 670

RESULT 5
OY 070608 PRELIMINARY: PRT: 752 AA.
AC 070608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
```

OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID-11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM87-2;
 RA MEDLINE-95127297; PubMed-7826699;
 RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM87-2;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12035; AAA76670.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00516; Gp120.1.
 DR Pfam: PF00517; Gp41.1.
 KW AIDS; Coat protein; glycoprotein; Polyprotein; Transmembrane.
 FT NON_TER
 SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 63.3%; Score 286; DB 15; Length 752;
 Best Local Similarity 98.1%; Pred. No. 9.6e-16;
 Matches 51; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWMREINNTSLHSLEESQNOEKNQELLEDKWSLMMNFI 52
 DB 624 NHTTWMREINNTSLHSLEESQNOEKNQELLEDKWSLMMNFI 675
 ID [1]
 AC Q90SM7; PRELIMINARY; PRT; 856 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID-11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HXB2;
 RA Altman-Onal Y., Cheynet V., Verrier B.;
 RT "Mutations and transcriptional alterations associated with the
 RT downregulation of HIV-1 envelope glycoprotein expression following
 RT acute cytopathic effects";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF358141; AAK4977.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; Gp120.
 DR Pfam: PF00516; Gp120.1.
 DR Pfam: PF00517; Gp41.1.
 KW AIDS; Coat protein; glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 856 AA; 97126 MW; 9458D02B2FD734B3 CRC64;

Query Match 63.1%; Score 285; DB 15; Length 856;
 Best Local Similarity 96.2%; Pred. No. 1.3e-15;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWMREINNTSLHSLEESQNOEKNQELLEDKWSLMMNFI 52
 DB 624 NHTTWMREINNTSLHSLEESQNOEKNQELLEDKWSLMMNFI 675
 ID [1]
 AC Q90SM7; PRELIMINARY; PRT; 856 AA.
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID-11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HXB2;
 RA Altman-Onal Y., Cheynet V., Verrier B.;
 RT "Mutations and transcriptional alterations associated with the
 RT downregulation of HIV-1 envelope glycoprotein expression following
 RT acute cytopathic effects";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF358141; AAK4977.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; Gp120.
 DR Pfam: PF00516; Gp120.1.
 DR Pfam: PF00517; Gp41.1.
 KW AIDS; Coat protein; glycoprotein; Polyprotein; Transmembrane.
 SQ SEQUENCE 856 AA; 97126 MW; 9458D02B2FD734B3 CRC64;

089797
 ID 089797; PRELIMINARY; PRT; 852 AA.
 AC 089797;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID-11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM90-2;
 RA MEDLINE-95127297; PubMed-7826699;
 RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB).";
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM90-2;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12053; AAA76685.1; -;
 DR EMBL: U12036; AAA76671.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; Gp120.
 DR Pfam: PF00516; Gp120.1.
 DR Pfam: PF00517; Gp41.1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
 KW Transmembrane.
 SQ SEQUENCE 852 AA; 96347 MW; 4E865229DAEB33CF CRC64;

Query Match 62.4%; Score 282; DB 15; Length 852;
 Best Local Similarity 96.2%; Pred. No. 2.3e-15;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWMREINNTSLHSLEESQNOEKNQELLEDKWSLMMNFI 52
 DB 620 NHTTWMREINNTSLHSLEESQNOEKNQELLEDKWSLMMNFI 671
 ID [1]
 AC Q92877; PRELIMINARY; PRT; 856 AA.
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID-57667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-9908984; PubMed-9882298;
 RA Cayabyab M., Karlsson G.B., Etemad-Moghadam B.A., Hofmann W.,
 RA Cayabaye T., Halloran M., Fantom J.W., Axelholm M.K., Letvin N.L.,
 RA Sodroski J.G.;
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
 RT responsible for the pathogenicity of a multiply passaged simian-human
 RT immunodeficiency virus (SHIV-HXB2).";
 RL J. Virol. 73:976-984(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Cayabyab M., Karlsson G.B., Etemad-Moghadam B., Hofmann W.,
 RA Halloran M., Axelholm M.W., Letvin N.L., Sodroski J.G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041850; AAD12142.1; -;
 DR InterPro: IPR000328; Env_Gp41.

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00517; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane.
 SQ SEQUENCE 856 AA; 97151 MW; C50B80388FB73659 CRC64;

Query Match 61.9%; Score 280; DB 15; Length 856;
 Best Local Similarity 63.5%; Pred. No. 3.4e-15;
 Matches 54; Conservative 9; Mismatches 10; Indels 12; Gaps 1;

OY 1 NHTTLEMDREINNTSLHSLSIESONQOEKNEDELELDKMASLWMMFN 52
 DB 624 NMTTMEWDREINNTSLHSLSIESONQOEKNEDELELDKMASLWMMFN 673

OY 61 IBEILSKYHIEHETARKKLLGER 85
 DB 674 --DITNMLYIKLIMYGVGLR 696

RESULT 9

OY93A6 PRELIMINARY; PRT; 645 AA.

AC 093A6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Truncated envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1007;
 RX MEDLINE=21192672; PubMed=11287644;
 RA Summan S., Lockey T.D., Slobod K.S., Jones B., Riberty J.M.,
 RA White S.W., Doherty P.C., Hurwitz J.L.;
 RT "Localization of CD4+ T cell epitope hotspots to exposed strands of
 RT HIV envelope glycoprotein suggests structural influences on antigen
 RT processing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).
 DR EMBL: AF321563; AAK18810.1; -
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00517; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 KM TRANSMEMBRANE.
 FT NON TER
 SQ SEQUENCE 645 AA; 72485 MW; B076514BE93362EC CRC64;

Query Match 61.3%; Score 277; DB 15; Length 645;
 Best Local Similarity 94.2%; Pred. No. 4.5e-15;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLHSLSIESONQOEKNEDELELDKMASLWMMFN 52
 DB 593 NMTTMEWDREINNTSLHSLSIESONQOEKNEDELELDKMASLWMMFN 644

RESULT 10

OY8243 PRELIMINARY; PRT; 851 AA.

AC 078243;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Env. polypeptide.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Carlini F., Federic M., Equestre M., Ricci S., Ratti G., Zibai Q.,
 RA Verani P., Rossi G.B.;
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer
 RT chronically infected HUT-78 cellular clone."
 RL J. Viral Diseases 1:40-55(1992).

[2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352106; PubMed=2765297;
 RA Federico M., Titti F., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Macchi B., Mangano N., Verani P., Rossi G.;
 RT "Biological and molecular characterization of producer and non
 RT producer clones from HUT-78 infected with a patient HIV isolate."
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).

[3]
 RP SEQUENCE FROM N.A.
 RA Titti F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Borsetti A., Saglio I., Verani P., Rossi G.;
 RT "Variability of HIV-1 virus: characteristics of an infected but not
 RT productive clone."
 RL Int. J. Immunopharmacol. 3:17-23(1990).

DR EMBL: 211530; CAAT7628.1; -
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00517; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B987E98027 CRC64;

Query Match 61.3%; Score 277; DB 15; Length 851;
 Best Local Similarity 94.2%; Pred. No. 5.9e-15;
 Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLHSLSIESONQOEKNEDELELDKMASLWMMFN 52
 DB 619 NMTTMEWDREINNTSLHSLSIESONQOEKNEDELELDKMASLWMMFN 670

RESULT 11

OY8582 PRELIMINARY; PRT; 854 AA.

AC 08582;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Envelope polypeptide.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86281827; PubMed=3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
 RA Martin M.A.;
 RT "Production of acquired immunodeficiency syndrome-associated
 RT retrovirus in human and nonhuman cells transfected with an infectious
 RT molecular clone."
 RL J. Virol. 59:284-291(1986).

[2]
 RP SEQUENCE FROM N.A.
 RP Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
 RL Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RP Buckler C.E.;
 RL Submitted (JUL-1989) to the EMBL/Genbank/DBJ databases.

[4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92219406; PubMed=1373204;
 RA Dai L.C., Litcau R., Takahashi K., Ennis F.A.;
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
 RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T

RT lymphocytes".
RL J. Virol. 66:3151-3154(1992).
DR EMBL: M19921; AAA44992.1; .
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120.1.
DR Pfam: PF00517; Gp41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D5595A CRC64;

Query Match 61.3%; Score 277; DB 15; Length 854;
Best Local Similarity 94.2%; Pred. No. 6e-15;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWEMDEINNTSLHSLEESONOQEKNEQELLEDKASLWNNFNI 52
DB 622 NNTWMEDEINNTSLHSLEESONOQEKNEQELLEDKASLWNNFNI 673

RESULT 12
ID 072502 PRELIMINARY; PRT; 854 AA.
AC 072502;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ENV Polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid-11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M4-3;
RX MEDLINE-96036482; PubMed-7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.,
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
from primary virus cultures using the polymerase chain reaction.";
RL Virology 213:80-86(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-M4-3;
RX MEDLINE-86281827; PubMed-3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
retrovirus in human and nonhuman cells transfected with an infectious
molecular clone.";
RL J. Virol. 59:284-291(1986).
DR EMBL: U26942; AAB60578.1; .
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120.1.
DR Pfam: PF00517; Gp41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT CONFLICT 214 H -> L (IN REF. 2).
FT CONFLICT 530 A -> S (IN REF. 2).
FT CONFLICT 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;

Query Match 61.3%; Score 277; DB 15; Length 854;
Best Local Similarity 94.2%; Pred. No. 6e-15;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWEMDEINNTSLHSLEESONOQEKNEQELLEDKASLWNNFNI 52
DB 622 NNTWMEDEINNTSLHSLEESONOQEKNEQELLEDKASLWNNFNI 673

RESULT 13
074599 PRELIMINARY; PRT; 856 AA.
ID 074599

AC 074599;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid-11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MCK1;
RX MEDLINE-90101366; PubMed-1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
(HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MCK1;
RA Iwataani Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86068; BAA12995.1; .
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120.1.
DR Pfam: PF00517; Gp41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C56685 CRC64;

Query Match 61.3%; Score 277; DB 15; Length 856;
Best Local Similarity 94.2%; Pred. No. 6e-15;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWEMDEINNTSLHSLEESONOQEKNEQELLEDKASLWNNFNI 52
DB 624 NNTWMEDEINNTSLHSLEESONOQEKNEQELLEDKASLWNNFNI 675

RESULT 14
ID 074090 PRELIMINARY; PRT; 856 AA.
AC 074090;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ENV.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid-11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PM213;
RX MEDLINE-90101366; PubMed-1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
(HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-PM213;
RA Iwataani Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86069; BAA13003.1; .
DR InterPro: IPR000328; Env_Gp41.
DR InterPro: IPR000777; Gp120.
DR Pfam: PF00516; Gp120.1.
DR Pfam: PF00517; Gp41.1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;

Query Match 61.3%; Score 277; DB 15; Length 856;

GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 25.1852 Seconds

(without alignments)
99.302 Million cell updates/sec

Title: US-09-877-606-4

Perfect score: 452
Sequence: 1 NHTTWLEMDREINNTSLIH.....SKYHIEHRIKRLIGER 85

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	64.2	138	4	US-09-570-921-20
2	290	64.2	138	4	US-09-570-921-21
3	290	64.2	268	4	US-08-965-056-16
4	290	64.2	345	4	US-09-272-342B-7
5	290	64.2	519	1	US-08-589-446-8
6	290	64.2	519	1	US-08-444-882-8
7	290	64.2	519	2	US-08-389-459A-8
8	290	64.2	519	3	US-08-987-867A-8
9	290	64.2	856	2	US-07-916-096A-2
10	290	64.2	856	2	US-09-337-387-11
11	278	61.5	839	4	US-08-472-240A-10
12	277	61.3	138	4	US-09-570-921-22
13	277	61.3	138	4	US-09-570-921-24
14	277	61.3	138	4	US-09-570-921-26
15	277	61.3	138	4	US-09-570-921-28
16	277	61.3	237	3	US-08-388-353-6A1
17	277	61.3	237	3	US-08-484-223B-90
18	277	61.3	268	4	US-08-965-056-17
19	277	61.3	268	4	US-08-965-056-18
20	277	61.3	282	5	PCT-US95-13335-1
21	277	61.3	338	3	US-08-486-099-90
22	277	61.3	338	3	US-08-360-107A-100
23	277	61.3	338	3	US-08-484-223B-90
24	277	61.3	338	3	US-08-919-597-90
25	277	61.3	338	3	US-08-475-668A-90
26	277	61.3	338	3	US-08-485-551A-90
27	277	61.3	338	3	US-08-471-913A-90

28	277	61.3	338	4	US-08-485-264A-90	Sequence 90, Appl
29	277	61.3	338	4	US-08-474-349A-90	Sequence 90, Appl
30	277	61.3	338	4	US-08-255-208A-26	Sequence 26, Appl
31	277	61.3	345	4	US-08-817-441-49	Sequence 49, Appl
32	277	61.3	615	4	US-09-257-490-11	Sequence 11, Appl
33	277	61.3	826	1	US-08-375-510-2	Sequence 2, Appl
34	277	61.3	826	2	US-08-487-657-23	Sequence 23, Appl
35	277	61.3	854	4	US-09-309-572-23	Sequence 9, Appl
36	277	61.3	856	4	US-09-124-900-9	Sequence 14, Appl
37	277	61.3	861	1	US-08-127-499A-14	Sequence 14, Appl
38	277	61.3	861	1	US-08-482-847-14	Sequence 10, Appl
39	277	61.3	861	4	US-07-956-483-16	Sequence 16, Appl
40	277	61.3	861	4	US-07-956-483-16	Sequence 1, Appl
41	277	61.3	861	4	US-08-472-240A-1	Sequence 7, Appl
42	277	61.3	861	4	US-08-472-240A-7	Sequence 103, Appl
43	277	61.3	861	4	US-08-817-441-103	Sequence 11, Appl
44	277	61.3	863	3	US-08-463-210-11	Sequence 7, Appl
45	277	61.3	880	2	US-08-788-815-7	

ALIGNMENTS

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RESULT 1
US-09-570-921-20
Sequence 20, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-20

Query Match      64.2%   Score 290; DB 4; Length 138;
Best Local Similarity 98.1%   Pred. No. 2e-22;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLIHSLIEESQOEKNEKDELDKRWASIMNFNI 52
DB 85 NHTTWLEMDREINNTSLIHSLIEESQOEKNEKDELDKRWASIMNFNI 136

RESULT 2
US-09-570-921-21
Sequence 21, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
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QY 1 NHTTWMREINNTSLHSLSIESQNOEKNEQLELDKWSIANNFNI 52
DB 420 NHTTWMREINNTSLHSLSIESQNOEKNEQLELDKWSIANNFNI 471

RESULT 6

US-08-444-882-8
Sequence 8, Application US/08444882
Patent No. 5622705
GENERAL INFORMATION:
APPLICANT: MORROW, Casey D.
TITLE OF INVENTION: ENCAPSATED POLIOVIRUS NUCLEIC
TITLE OF INVENTION: ACID AND METHODS OF MAKING AND
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,882
FILING DATE: 19-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Geary III, William C.
REGISTRATION NUMBER: 31,359
REFERENCE/DOCKET NUMBER: DAG-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-444-882-8

Query Match 64.2%; Score 290; DB 1; Length 519;
Best Local Similarity 98.1%; Pred. No. 9.3e-22;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWMREINNTSLHSLSIESQNOEKNEQLELDKWSIANNFNI 52
DB 420 NHTTWMREINNTSLHSLSIESQNOEKNEQLELDKWSIANNFNI 471

RESULT 7

US-08-389-459A-8
Sequence 8, Application US/08389459A
Patent No. 5817512
GENERAL INFORMATION:
APPLICANT: MORROW, Casey D. and Porter, Donna, C.
TITLE OF INVENTION: ENCAPSATED RECOMBINANT POLIOVIRUS
TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,459A
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Silveri, Jean M.
REGISTRATION NUMBER: 39,030
REFERENCE/DOCKET NUMBER: DAG-004CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-389-459A-8

Query Match 64.2%; Score 290; DB 2; Length 519;
Best Local Similarity 98.1%; Pred. No. 9.3e-22;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWMREINNTSLHSLSIESQNOEKNEQLELDKWSIANNFNI 52
DB 420 NHTTWMREINNTSLHSLSIESQNOEKNEQLELDKWSIANNFNI 471

US-08-987-867A-8
Sequence 8, Application US/08987867A
Patent No. 6063384
GENERAL INFORMATION:
APPLICANT: C. Morrow et al.
TITLE OF INVENTION: ENCAPSATED RECOMBINANT VIRAL
TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,867A
FILING DATE: 09-DEC-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: DAG-004CPDV
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-987-867A-8

Query Match 64.2%; Score 290; DB 3; Length 519;
Best Local Similarity 98.1%; Pred. No. 9,3e-22;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNTYSLIHSIESONQOEKNEDELLELDKWSLMMWNI 52
DB 420 NHTTWLMDREINNTYSLIHSIESONQOEKNEDELLELDKWSLMMWNI 471

RESULT 9
US-07-916-098A-2
Sequence 2, Application US/07916098A
Patent No. 5871732

GENERAL INFORMATION:

APPLICANT: BURRY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843

FILING DATE: No. 5871732ember 27, 1991

CLASSIFICATION: 424

FILING DATE: No. 5871732ember 27, 1990

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL

REGISTRATION NUMBER: 26,949

REFERENCE/DOCKET NUMBER: 92,310-G

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000

TELEFAX: (312) 715-1234

TELEX: 910/221-5317

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 856 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 64.2%; Score 290; DB 2; Length 856;
Best Local Similarity 98.1%; Pred. No. 1.7e-21;

Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 NHTTWLMDREINNTYSLIHSIESONQOEKNEDELLELDKWSLMMWNI 52
DB 624 NHTTWLMDREINNTYSLIHSIESONQOEKNEDELLELDKWSLMMWNI 675

RESULT 10
US-09-337-387-11
Sequence 11, Application US/09337387
Patent No. 6420545

GENERAL INFORMATION:

APPLICANT: HOXIE, James A.
APPLICANT: LABRANCHE, Celia C.
APPLICANT: DOMS, Robert W.
APPLICANT: HOFFMAN, Trevor L.
TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND
TITLE OF INVENTION: THERAPEUTICS
FILE REFERENCE: Hoxie 9596-10401 (0282)
CURRENT APPLICATION NUMBER: US/09/337,387
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/317,556
PRIOR FILING DATE: 1999-05-24
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 856
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-337-387-11

Query Match 64.2%; Score 290; DB 4; Length 856;
Best Local Similarity 98.1%; Pred. No. 1.7e-21;
Matches 51; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNTYSLIHSIESONQOEKNEDELLELDKWSLMMWNI 52
DB 624 NHTTWLMDREINNTYSLIHSIESONQOEKNEDELLELDKWSLMMWNI 675

RESULT 11

US-08-472-240A-10

Sequence 10, Application US/08472240A

Patent No. 6284248

GENERAL INFORMATION:

APPLICANT: KIENY, Marie-Paule

TITLE OF INVENTION: NOVEL HYBRID, SOLUBLE AND UNCLEAVED

TITLE OF INVENTION: 9P160 VARIANT

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SNECKER & MATHIS

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,240A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,483

FILING DATE: 31-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 017753-055

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 839 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-240A-10

Query Match
Best Local Similarity 61.3%; Score 277; DB 4; Length 839;
Best Local Similarity 68.0%; Pred. No. 2.6e-20;
Matches 51; Conservative 8; Mismatches 4; Indels 12; Gaps 1;

QY 1 NHTTWLEMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 60
DB 629 NNTWTWMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI----- 679

QY 61 IEELSKTYHENEI 75
DB 680 ---ITWMLWYIKNRV 691

RESULT 12
US-09-570-921-22
Sequence 22, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-22

Query Match
Best Local Similarity 61.3%; Score 277; DB 4; Length 138;
Best Local Similarity 94.2%; Pred. No. 4.2e-21;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 52
DB 85 NNTWTWMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 136

RESULT 13
US-09-570-921-24
Sequence 24, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24

LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-24

Query Match
Best Local Similarity 61.3%; Score 277; DB 4; Length 138;
Best Local Similarity 94.2%; Pred. No. 4.2e-21;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 52
DB 85 NNTWTWMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 136

RESULT 14
US-09-570-921-26
Sequence 26, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-26

Query Match
Best Local Similarity 61.3%; Score 277; DB 4; Length 138;
Best Local Similarity 94.2%; Pred. No. 4.2e-21;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 52
DB 85 NNTWTWMDREINNYTSLHSLEESONOEKNEOELELDKVASLMMWNI 136

RESULT 15
US-09-570-921-58
Sequence 58, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 58
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-58

Query Match
Best Local Similarity 61.3%; Score 277; DB 4; Length 138;
Best Local Similarity 94.2%; Pred. No. 4.2e-21;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Wed May 7 14:34:27 2003

us-09-877-606-4.rai

Page 6

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0Y      1 NHTTTEEMREINNNTSLHSLEESONQOQKNEOLLELKKASIMAMNT 52
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Db      85 NNHTTWEMREINNNTSLHSLEESONQOQKNEOLLELKKASIMAMNT 136

Search completed: May 7, 2003, 09:59:49
Job time : 25.1852 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 46.8287 Seconds
(without alignments)
167.038 Million cell updates/sec

Title: US-09-877-606-4

Perfect score: 452
Sequence: 1 NHTTWLEMDREINNTSLIH.....SKYHENEIRIKRIGER 85

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA.*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	64.2	268	10	US-09-854-816-16 Sequence 16, Appl
2	290	64.2	344	9	US-10-040-349B-1 Sequence 1, Appl
3	290	64.2	519	10	US-09-756-551A-8 Sequence 8, Appl
4	290	64.2	856	9	US-09-476-242-1 Sequence 1, Appl
5	278	61.3	177	9	US-10-040-349B-2 Sequence 2, Appl
6	277	61.3	56	10	US-09-779-451-4 Sequence 4, Appl
7	277	61.3	221	9	US-10-059-271-84 Sequence 84, Appl
8	277	61.3	232	9	US-10-059-271-81 Sequence 81, Appl
9	277	61.3	254	9	US-10-059-271-82 Sequence 82, Appl
10	277	61.3	268	9	US-10-059-271-97 Sequence 97, Appl
11	277	61.3	268	10	US-09-854-816-17 Sequence 17, Appl
12	277	61.3	268	9	US-09-854-816-18 Sequence 18, Appl
13	277	61.3	345	9	US-10-026-741-49 Sequence 49, Appl
14	277	61.3	345	10	US-09-779-451-8 Sequence 8, Appl
15	277	61.3	391	9	US-10-059-271-93 Sequence 93, Appl
16	277	61.3	853	9	US-10-003-035-33 Sequence 33, Appl
17	277	61.3	861	9	US-10-026-741-103 Sequence 103, Appl
18	277	61.3	1101	9	US-10-003-035-53 Sequence 53, Appl
19	277	61.3	1186	9	US-10-003-035-55 Sequence 55, Appl

20	274	60.6	268	10	US-09-854-816-19 Sequence 19, Appl
21	260	57.5	268	10	US-09-854-816-13 Sequence 13, Appl
22	260	57.5	269	10	US-09-854-816-46 Sequence 46, Appl
23	256	56.6	46	10	US-09-779-451-41 Sequence 41, Appl
24	255	56.4	269	10	US-09-854-816-43 Sequence 43, Appl
25	254	56.2	268	10	US-09-854-816-9 Sequence 9, Appl
26	253	56.0	269	10	US-09-854-816-12 Sequence 12, Appl
27	252	55.8	268	10	US-09-854-816-26 Sequence 26, Appl
28	252	55.8	269	10	US-09-854-816-28 Sequence 28, Appl
29	252	55.8	847	10	US-09-476-242-2 Sequence 2, Appl
30	251	55.5	233	10	US-09-854-816-50 Sequence 50, Appl
31	251	55.5	619	10	US-09-891-609-4 Sequence 4, Appl
32	251	55.5	646	10	US-09-891-609-2 Sequence 2, Appl
33	248	54.9	269	10	US-09-854-816-44 Sequence 44, Appl
34	247	54.6	268	10	US-09-854-816-8 Sequence 8, Appl
35	247	54.6	269	10	US-09-854-816-41 Sequence 41, Appl
36	247	54.6	579	9	US-10-032-162-15 Sequence 15, Appl
37	247	54.6	625	9	US-10-032-162-17 Sequence 17, Appl
38	247	54.6	633	9	US-10-032-162-13 Sequence 13, Appl
39	246	54.4	269	10	US-09-854-816-42 Sequence 42, Appl
40	245	54.2	269	10	US-09-854-816-32 Sequence 32, Appl
41	245	54.2	269	10	US-09-854-816-34 Sequence 34, Appl
42	244	54.0	267	10	US-09-854-816-38 Sequence 38, Appl
43	243	53.8	269	10	US-09-854-816-15 Sequence 15, Appl
44	243	53.8	269	10	US-09-854-816-45 Sequence 45, Appl
45	242	53.5	269	10	US-09-854-816-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-854-816-16
; Sequence 16, Application us/09854816
; Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovastnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:

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RESULT 5
US-10-040-349B-2
; Sequence 2, Application US/10040349B

Publication No. US20030082521A1
GENERAL INFORMATION:
APPLICANT: Brasseur, Robert
APPLICANT: Charlotiaux, Benoit
APPLICANT: Chevalier, Michel
APPLICANT: El Hadid, Raphaelle
APPLICANT: Krell, Tino
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
FILE REFERENCE: 01-078-A
CURRENT APPLICATION NUMBER: US/10/040,349B
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 177
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
NAME/KEY: Peptide
LOCATION: (1)..(177)
OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2

Query Match 61.5%; Score 278; DB 9; Length 177;
Best Local Similarity 68.0%; Pred. No. 1.5e-19;
Matches 51; Conservative 8; Mismatches 4; Indels 12; Gaps 1;

OY 1 NHTTWLEMDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 60
DB 90 NNTWMEWDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI----- 140
OY 61 IEELSKYHENEI 75
DB 141 ---ITWMLWYIKNRV 152

RESULT 6
US-09-779-451-4
Sequence 4, Application US/09779451
Patent No. US20020094521A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: US 60/181,543
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4

Query Match 61.3%; Score 277; DB 10; Length 56;
Best Local Similarity 94.2%; Pred. No. 5.2e-20;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 52
DB 2 NNTWMEWDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 53

RESULT 7
US-10-059-271-84
Sequence 84, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:

APPLICANT: REPEKE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84
LENGTH: 221
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84

Query Match 61.3%; Score 277; DB 9; Length 221;
Best Local Similarity 94.2%; Pred. No. 2.4e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 52
DB 117 NNTWMEWDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 168

RESULT 8
US-10-059-271-81
Sequence 81, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPEKE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 81
LENGTH: 232
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-81

Query Match 61.3%; Score 277; DB 9; Length 232;
Best Local Similarity 94.2%; Pred. No. 2.5e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 52
DB 130 NNTWMEWDREINNTYSLHSLIEESQNOEKNEQLELDKASLMMNFNI 181

RESULT 9
US-10-059-271-82
Sequence 82, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPEKE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN

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; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-82

Query Match      61.3%; Score 277; DB 9; Length 254;
Best Local Similarity 94.2%; Pred. No. 2.7e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTLEMDREINNTSLIHSIESQNOQEKNEQELLELDKWSLMMWFI 52
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DB 152 NMTWMEWDREINNTSLIHSIESQNOQEKNEQELLELDKWSLMMWFI 203

RESULT 10
US-10-059-271-97
; Sequence 97, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; TITLE OF INVENTION: BEING IMMOBILIZED
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 97
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-059-271-97

Query Match      61.3%; Score 277; DB 9; Length 256;
Best Local Similarity 94.2%; Pred. No. 2.8e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTLEMDREINNTSLIHSIESQNOQEKNEQELLELDKWSLMMWFI 52
; :|:|||||
DB 152 NMTWMEWDREINNTSLIHSIESQNOQEKNEQELLELDKWSLMMWFI 203

RESULT 11
US-09-854-816-17
; Sequence 17, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
```

```

; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-854-816-17

Query Match      61.3%; Score 277; DB 10; Length 268;
Best Local Similarity 94.2%; Pred. No. 2.9e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTLEMDREINNTSLIHSIESQNOQEKNEQELLELDKWSLMMWFI 52
; :|:|||||
DB 154 NMTWMEWDREINNTSLIHSIESQNOQEKNEQELLELDKWSLMMWFI 205

RESULT 12
US-09-854-816-18
; Sequence 18, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match 61.3%; Score 277; DB 10; Length 268;
Best Local Similarity 94.2%; Pred. No. 2,9e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLHSLSIESQNOQEKNEQELLELDKWSIMNFI 52
DB 154 NNMTWMEWDREINNTSLHSLSIESQNOQEKNEQELLELDKWSIMNFI 205

RESULT 13
US-10-026-741-49

Sequence 49, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:

APPLICANT: CHARNEAU, PIERRE
CLAVEL, FRANCOISE
BORMAN, ANDREW
OUILLENT, CAROLINE
GUETARD, DENISE
MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-AUG-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Query Match 61.3%; Score 277; DB 9; Length 345;
Best Local Similarity 94.2%; Pred. No. 3,8e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLHSLSIESQNOQEKNEQELLELDKWSIMNFI 52
DB 113 NNMTWMEWDREINNTSLHSLSIESQNOQEKNEQELLELDKWSIMNFI 164

RESULT 14
US-09-779-451-8

Sequence 8, Application US/09779451
Patent No. US20020094521A1
GENERAL INFORMATION:

APPLICANT: Wild, Carl T.
APPLICANT: Allaway, Graham P.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.030003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 345
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-8

Query Match 61.3%; Score 277; DB 10; Length 345;
Best Local Similarity 94.2%; Pred. No. 3,8e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLHSLSIESQNOQEKNEQELLELDKWSIMNFI 52
DB 113 NNMTWMEWDREINNTSLHSLSIESQNOQEKNEQELLELDKWSIMNFI 164

RESULT 15
US-10-059-271-93

Sequence 93, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPE, HEINRICH
APPLICANT: BUDE, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 93
LENGTH: 391
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-93

Query Match 61.3%; Score 277; DB 9; Length 391;
Best Local Similarity 94.2%; Pred. NO. 4.4e-19;
Matches 49; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTLEMDREINNTSLIHSLESQNOQEKNEQELLELDKWSIWMFNI 52
DB 155 NMTTWMEDREINNTSLIHSLESQNOQEKNEQELLELDKWSIWMFNI 206

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Job time : 47.8287 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:40:21 ; Search time 6.38426 Seconds

(without alignments)
146.102 Million cell updates/sec

Title: US-09-877-606-5

Perfect score: 48

Sequence: 1 LMNMFDI 7

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	48	100.0	8	22	ABP15182
3	48	100.0	8	22	ABP18560
4	48	100.0	9	22	ABP12213
5	48	100.0	9	22	ABP17691
6	48	100.0	10	22	ABP12373
7	48	100.0	10	22	ABP17694
8	48	100.0	11	22	ABP12500
9	48	100.0	15	16	AA68688
10	48	100.0	15	18	AAW23658

11	48	100.0	15	19	AAW67374	HIV-1 peptide epit
12	48	100.0	15	20	AAV39707	HIV1 chimeric pept
13	48	100.0	15	20	AAW99908	HIV-1 vaccine synt
14	48	100.0	18	16	AA68686	CLTB-94 B-cell epi
15	48	100.0	18	16	AAW25856	HIV-1 T/B cell epi
16	48	100.0	18	19	AAW67372	HIV-1 peptide epit
17	48	100.0	18	20	AAV39705	HIV1 chimeric pept
18	48	100.0	18	20	AAW99907	HIV-1 vaccine synt
19	48	100.0	20	17	AA68684	CLTB-92A B-cell ep
20	48	100.0	20	17	AAW08066	HIV peptide #51.
21	48	100.0	20	18	AAW25854	HIV-1 T/B cell epi
22	48	100.0	20	19	AAW67370	HIV-1 peptide epit
23	48	100.0	20	20	AAV39703	HIV1 chimeric pept
24	48	100.0	20	20	AAW99906	HIV-1 vaccine synt
25	48	100.0	30	16	AA68687	P24E/CLTB-96 chime
26	48	100.0	30	18	AAW25857	HIV-1 T/B cell epi
27	48	100.0	30	19	AAW67373	HIV-1 peptide epit
28	48	100.0	30	20	AAV39706	HIV1 chimeric pept
29	48	100.0	30	20	AAW99979	HIV-1 vaccine synt
30	48	100.0	32	16	AAW77737	P24E/CLTB-96 chime
31	48	100.0	33	16	AA68685	HIV-1 T/B cell epi
32	48	100.0	33	18	AAW25855	HIV-1 peptide epit
33	48	100.0	33	19	AAW67371	HIV1 chimeric pept
34	48	100.0	33	20	AAV39704	HIV-1 vaccine synt
35	48	100.0	33	20	AAW99908	HIV-1 vaccine synt
36	48	100.0	35	16	AA68683	P24E/CLTB-92A chime
37	48	100.0	35	16	AAW77735	HIV-1 T/B cell epi
38	48	100.0	35	19	AAW25853	HIV-1 peptide epit
39	48	100.0	35	19	AAW67369	HIV1 chimeric pept
40	48	100.0	35	20	AAV39702	HIV-1 vaccine synt
41	48	100.0	35	20	AAW99977	P24E/CLTB-92A chime
42	48	100.0	37	16	AAW77733	HIV group M/ group
43	48	100.0	149	21	AAW12262	Anti-HIV-1 group O
44	48	100.0	167	19	AAW69320	HIV-1 gp41 glycopr
45	48	100.0	170	22	AAW61503	

ALIGNMENTS

RESULT 1
ABP12066
ID ABP12066 standard; Peptide; 8 AA.
XX
AC ABP12066;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #123.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN W0200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000MO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

XX Claim 32; Page 116; 448bp; English.

PS The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention.

SQ Sequence 8 AA;

XX

Query Match 100.0%; Score 48; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LWNWFDI 7

DB 2 LWNWFDI 8

RESULT 2

ABP15182

ID ABP15182 standard; Peptide: 8 AA.

XX

AC ABP15182;

XX

DT 15-JUL-2002 (first entry)

XX

DE HIV A24 super motif env peptide #62.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KM vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US27766.

XX

PR 05-OCT-1999; 99US-0412863.

XX

PA (EPI-M-) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cells E, Kudo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PS peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 180; 448bp; English.

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

CC may be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or

CC tumour-associated antigens, which therefore reduces the likelihood of

CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability

CC to combine selected groups (CTL and HTL), and further, to modify the

CC composition of the groups, achieving, for example, enhanced

CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412

CC represent peptide sequences used in the exemplification of the present

CC invention.

SQ Sequence 8 AA;

XX

Query Match 100.0%; Score 48; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LWNWFDI 7

DB 2 LWNWFDI 8

RESULT 3

ABP18560

ID ABP18560 standard; Peptide: 8 AA.

XX

AC ABP18560;

XX

DT 15-JUL-2002 (first entry)

XX

DE HIV B62 super motif env peptide #135.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KM vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;

KW antigen; vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus type 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US27766.

XX

PR 05-OCT-1999; 99US-0412863.

XX

PA (EPI-M-) EPIMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Cells E, Kudo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PS peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 249; 448bp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 48; DB 22; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LWNMFEDI 7
| | | | | | |
Db 2 LWNMFEDI 8

RESULT 4
ABP12213
ID ABP12213 standard; Peptide; 9 AA.

XX AC ABP12213;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A02 super motif env peptide #270.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPI-M-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 119; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABP25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,

CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LWNMFEDI 7
| | | | | | |
Db 2 LWNMFEDI 8

RESULT 5
ABP17691
ID ABP17691 standard; Peptide; 9 AA.

XX AC ABP17691;

XX DT 15-JUL-2002 (first entry)

XX DE HIV B58 super motif env peptide #92.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.

XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPI-M-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 231; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABP25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,

Query Match	Similarity	Score	DB	Length
Best Local	100.0%	100.0%	Pred. No. 7.8e+05;	
Matches	7;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
1	LNMFEDI 7			
3	LNMFEDI 9			
RESULT 6				
ABP12373				
ABP12373	standard; Peptide; 10 AA.			
ABP12373;				
15-JUL-2002	(first entry)			
HIV A02 super motif env peptide #430.				
HIV_ HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.				
Human immunodeficiency virus type 1.				
WO200124810-A1.				
12-APR-2001.				
05-OCT-2000; 2000WO-US27766.				
05-OCT-1999; 99US-0412863.				
(EPLM-) EPRIMONE INC.				
Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R; Baker DM, Celis E, Kubo RT, Grey HM; WPI; 2001-354887/37.				
Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.				
Claim 32; Page 122; 448pp; English.				
The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of				

CC	escape mutants. Furthermore, immunosuppressive groups that may be present
CC	in whole antigens can be avoided with the use of group-based vaccines.
CC	An additional advantage of an group-based vaccine approach is the ability
CC	to combine selected groups (CTL and HTL), and further, to modify the
CC	composition of the groups, achieving, for example, enhanced
CC	immunogenicity. Accordingly, the immune response can be modulated, as
CC	appropriate, for the target disease. Similar engineering of the response
CC	is not possible with traditional approaches. ABP11501 to ABP25412
CC	represent peptide sequences used in the exemplification of the present
CC	invention.
XX	
SQ	Sequence 10 AA;
OY	
DB	
Query Match	100.0%; Score 48; DB 22; Length 10;
Best Local Similarity	100.0%; Pred. No. 0.18;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 LMNWFDI 7	
4 LMNWEDI 10	
RESULT 7	
ID	ABP17694 standard; Peptide: 10 AA.
AC	ABP17694;
DT	15-JUL-2002 (first entry)
DE	HIV B58 super motif env peptide #95.
XX	
KW	HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KM	vpu; vif; tat; cytoxic T lymphocyte; CTL; Immune response; epitope;
KV	antigen; vaccine; HIV infection; Immunisation; virucide.
XX	
OS	Human immunodeficiency virus type 1.
PN	WO200124810-A1.
PD	12-APR-2001.
PE	05-OCT-2000; 2000MO-US27766.
PR	05-OCT-1999; 99US-0412863.
PA	(EPIM-) EPIMUNE INC.
PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI	Baker DM, Cells E, Kudo RT, Grey HM;
DR	WPI; 2001-354887/37.
Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)	
peptide groups, useful for vaccinating against HIV-1 -	
Claim 32; Page 231; 448pp; English.	
The present invention describes a composition (I) comprising a prepared	
human immunodeficiency virus-1 (HIV-1) group comprising an amino acid	
sequence selected from 51 defined amino acid sequences (AB125347 to	
ABP25397). (I) has virucide activity and can be used in vaccines. (I)	
may be used for immunising subjects against HIV-1 infections. The use of	
group-based vaccines has several advantages over traditional vaccines,	
particularly when compared to the use of whole antigens in vaccine	
compositions. There is evidence that the immune response to whole	
antigens is directed largely toward variable regions of the antigen,	
allowing for immune escape due to mutations. The groups for inclusion in	
tumour-associated vaccine may be selected from conserved regions of viral or	
escape mutants. Furthermore, immunosuppressive groups that may be present	
in whole antigens can be avoided with the use of group-based vaccines.	
An additional advantage of an group-based vaccine approach is the ability	

CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX Sequence 10 AA;

Query Match 100.0%; Score 48; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.18; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;
QY 1 LAMNFDI 7
| | | | |
DB 4 LAMNFDI 10

RESULT 8

ABP12500 standard; Peptide; 11 AA.

XX ABP12500;

DT 15-JUL-2002 (first entry)

DE HIV A02 super motif env peptide #557.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr;

KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;

XX antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.

PN WO200124810-A1.

PD 12-APR-2001.

PF 05-OCT-2000; 2000WO-US27766.

XX 05-OCT-1999; 99US-0412863.

PA (EPIM-) EPIMONE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX Baker DM, Cells E, Kubo RT, Grey HM;

PT WPI; 2001-354867/37.

PS Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

XX peptide groups, useful for vaccinating against HIV-1 -

XX Claim 32; Page 125; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABU25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as

CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX Sequence 11 AA;

Query Match 100.0%; Score 48; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;
QY 1 LAMNFDI 7
| | | | |
DB 4 LAMNFDI 10

RESULT 9

AAR6868 standard; peptide; 15 AA.

XX AAR6868;

DT 07-SEP-1995 (first entry)

DE CLTB-96 B-cell epitope.

XX T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen;

KW gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.

XX Human immunodeficiency virus type 1.

PN WO9429339-A.

PD 22-DEC-1994.

PF 08-JUN-1994; 94WO-CA00317.

XX 09-JUN-1993; 93US-0073378.

PA (CONN-) CONNAUGHT LAB LTD.

PI Chong P, Klein MH, Sla CDY;

XX WPI; 1995-036400/05.

PT Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell

XX epitope of gag protein linked to B-cell epitope of V3 loop

PS Claim 4; Page 42; 69pp; English.

CC This sequence represents the B-cell epitope, CLTB-96, which contains
CC the gp41 neutralising epitope EUDKWA. This peptide is pref. linked
CC to the T-cell epitope, p24E, in the production of a chimeric peptide.
CC Chimeric peptides such as this are recognised by monoclonal antibody
CC 2F5. These chimeric peptides may then be used in the production of
CC HIV-1 vaccines. These peptide sequences may also be used in the
CC production of multimeric peptides in which the peptides are C-
CC terminally modified by the addition of a lys residue which is modified
CC on its epsilon TCC amino acid to carry an additional copy of the
CC peptide molecule. The linear and multimeric peptides may be used for
CC the treatment of AIDS by acting to displace the binding of HIV virus
CC to human or animal cells or by disturbing the 3D organisation of the
CC virus.

XX Sequence 15 AA;

Query Match 100.0%; Score 48; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;
QY 1 LAMNFDI 7
| | | | |

DB 8 LMNWEDI 14

RESULT 10
AAW25858
ID AAW25858 standard; peptide; 15 AA.
XX
AC AAW25858;
XX
DT 20-OCT-1997 (first entry)
XX
DE HIV-1 T/B cell epitope CTLB-96 contains gp41 neutralisation epitope.
XX
KW HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
XX V3 loop; vaccine; determinant; chimeric.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..6
FT /note= "gp41 neutralisation epitope"
XX
PN US5639854-A.
XX
PD 17-JUN-1997.
XX
PF 09-JUN-1993; 93US-0073378.
XX
PR 09-JUN-1994; 94US-0257528.
PR 09-JUN-1993; 93US-0073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Chong P, Klein MH, Sia CDY;
XX
DR WPI: 1997-332082/30.
XX
PT Tandem synthetic HIV peptide(s) useful as immunogens - comprising
XX gag protein T-cell epitope linked to env protein B-cell epitope
XX
PS Example 1; Column 21-22; 41pp; English.
XX
CC The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAT, IIB, RF, Z6, 2054,
CC 1714 and BX08. The peptides are chimeric and can be linked to a
CC branched lys backbone. The peptides AAW25853-67 represents chimeric
CC T/B cell epitope peptides which also contain a gp41 neutralisation
CC epitope.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 48; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWEDI 7
DB 8 LMNWEDI 14

RESULT 11
AAW67374
ID AAW67374 standard; peptide; 15 AA.
XX
AC AAW67374;
XX
DT 25-JAN-1999 (first entry)

XX
DE HIV-1 peptide epitope CTLB-96.
XX
KW Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
XX V3 loop; gp41.
XX
OS Human immunodeficiency virus type 1.
XX
PN US5817754-A.
XX
PD 06-OCT-1998.
XX
PF 05-JUN-1995; 95US-0464329.
XX
PR 09-JUN-1994; 94US-0257528.
PR 09-JUN-1993; 93US-0073378.
PR 05-JUN-1995; 95US-0464329.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Chong P, Klein MH, Sia CDY;
XX
DR WPI: 1998-556461/47.
XX
PT Synthetic human immunodeficiency virus-1 peptide(s) - containing
PT T-cell epitope and B-cell epitope(s) are candidate vaccines against
PT HIV-1
XX
PS Disclosure; Column 21-22; 40pp; English.
XX
CC The invention relates to a novel immunogenic composition for use in
CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
CC are generally designed based on the P24 core protein and the B-cell
CC epitopes from the V3 loop of the gp120 protein from various HIV-1
CC strains. This peptide corresponds to an HIV-1 gp41 protein epitope.
CC The peptide is used to generate the hybrid epitope AAW67373.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 48; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWEDI 7
DB 8 LMNWEDI 14

RESULT 12
AAV39707
ID AAV39707 standard; peptide; 15 AA.
XX
AC AAV39707;
XX
DT 26-NOV-1999 (first entry)
XX
DE HIV1 chimeric peptide CTLB-96.
XX
KW HIV; vaccine; immunogenic composition; T cell epitope; B cell epitope;
XX infection; antibody; antiviral.
XX
OS Human immunodeficiency virus type 1.
XX
PN US5951986-A.
XX
PD 14-SEP-1999.
XX
PF 06-JUN-1995; 95US-0467881.
XX
PR 09-JUN-1994; 94US-0257528.
PR 09-JUN-1993; 93US-0073378.
XX

PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Klein MH, Chong P, Sia CDY;
 XX
 DR WPI; 1999-550482/46.
 XX
 PT Immunogenic composition containing synthetic fusion polypeptides
 PT containing both the T and B cell epitopes of the human immunodeficiency
 XX virus, useful antigens in producing vaccines
 XX
 PS Example 1; Column 23-24; 43pp; English.
 XX
 CC This sequence represents a fragment of a HIV1 protein, and can be used in
 CC the immunogenic composition of the invention. The composition comprises a
 CC synthetic fusion polypeptide which includes a sequence encoding 1 or more
 CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
 CC carrier. Both the T cell and B cell epitopes are derived from HIV
 CC proteins. The compositions are useful as vaccines against HIV infection.
 CC The composition induces HIV-1-specific polyclonal antibodies that are
 CC opsonising and antiviral. The peptide components may be selected to
 CC induce a response against different viral isolates and in subjects who
 CC recognise different T cell epitopes.
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 48; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LNMWFDI 7
 DB 8 LNMWFDI 14
 RESULT 13
 AAW99908
 ID AAW99908 standard; peptide; 15 AA.
 XX
 AC AAW99908;
 XX
 DT 05-MAY-1999 (first entry)
 XX
 DE HIV-1 vaccine synthetic peptide CLTB-96.
 XX
 KW HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
 KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus type 1.
 OS
 XX US5876731-A.
 PN
 PD 02-MAR-1999.
 XX
 PF 05-JUN-1995; 95US-0462507.
 XX
 PR 09-JUN-1994; 94US-0257528.
 PR 09-JUN-1993; 93US-0073378.
 PR 05-JUN-1995; 95US-0462507.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Chong P, Klein MH, Sia CDY;
 XX
 DR WPI; 1999-189590/16.
 XX
 PT Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
 PT epitope linked to gp41 B-cell epitope
 XX
 PS Claim 7; Column 72; 41pp; English.
 CC The present invention describes a synthetic peptide comprising an amino
 CC acid sequence containing a T-cell epitope of an HIV gag protein linked

CC at its C terminus to an amino acid sequence containing a B-cell epitope
 CC of an HIV gp41 protein and containing the amino acid sequence:
 CC X1LKDMX2; where X1 = E, A, G or Q, and X2 = A or T, or an amino acid
 CC sequence capable of eliciting an HIV-specific antiserum and recognizing
 CC the sequence X1LKDMX2. The synthetic peptide is useful in vaccines
 CC against HIV infection and in diagnostic applications. AAW8892 to
 CC AAW99906, and AAW99899 to AAW9989 represent synthetic peptides from the
 CC present invention.
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 48; DB 20; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LNMWFDI 7
 DB 8 LNMWFDI 14
 RESULT 14
 AAR68686
 ID AAR68686 standard; peptide; 18 AA.
 XX
 AC AAR68686;
 XX
 DT 07-SEP-1995 (first entry)
 XX
 DE CLTB-94 B-cell epitope.
 XX
 KW T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen;
 KW gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.
 XX
 OS Human immunodeficiency virus type 1.
 OS
 XX WO9429339-A.
 PN
 PD 22-DEC-1994.
 XX
 PF 08-JUN-1994; 94WO-CA00317.
 XX
 PR 09-JUN-1993; 93US-0073378.
 XX
 PA (CONN-) CONNAUGHT LAB LTD.
 XX
 PI Chong P, Klein MH, Sia CDY;
 XX
 DR WPI; 1995-036400/05.
 XX
 PT Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell
 PT epitope of gag protein linked to B-cell epitope of V3 loop
 PT protein of an HIV-1 isolate
 XX
 PS Claim 4; Page 42; 69pp; English.
 XX
 CC This sequence represents the B-cell epitope, CLTB-94, which contains
 CC the gp41 neutralising epitope ELDKWA. This peptide is pref. linked
 CC to the T-cell epitope, p24E, in the production of a chimeric peptide.
 CC Chimeric peptides such as this are recognised by monoclonal antibody
 CC 2F5. These chimeric peptides may then be used in the production of
 CC HIV-1 vaccines. These peptide sequences may also be used in the
 CC production of multimeric peptides in which the peptides are C-
 CC terminally modified by the addition of a lys residue which is modified
 CC on its epsilon RCC amino acid to carry an additional copy of the
 CC peptide molecule. The linear and multimeric peptides may be used for
 CC the treatment of AIDS by acting to displace the binding of HIV virus
 CC to human or animal cells or by disturbing the 3D organisation of the
 CC virus.
 CC
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 48; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.33;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7
 |||||
 Db 11 LMNMFPI 17

RESULT 15
 AAW25856

ID AAW25856 standard; peptide; 18 AA.

XX AAW25856;

AC AAW25856;

XX 20-OCT-1997 (first entry)

DE HIV-1 T/B cell epitope CTLB-94 contains gp41 neutralisation epitope.

XX HIV: human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;

XX V3 loop; vaccine; determinant; chimeric.

XX Synthetic.

XX Key

XX Region

XX Location/Qualifiers

XX 4..9

XX /note= "gp41 neutralisation epitope"

XX US5639854-A.

XX 17-JUN-1997.

XX 09-JUN-1993; 93US-0073378.

XX 09-JUN-1994; 94US-0257528.

XX 09-JUN-1993; 93US-0073378.

XX (CONN-) CONNAUGHT LAB LTD.

XX Chong P, Klein MH, Sia CD;

XX WPI; 1997-332082/30.

XX Tandem synthetic HIV peptide(s) useful as immunogens - comprising

XX gag protein T-cell epitope linked to env protein B-cell epitope

XX Example 1; Column 21-22; 41p; English.

XX The invention relates to new synthetic peptides comprising at least one

XX amino acid sequence comprising an HIV gag protein T-cell epitope linked

XX at its C- or N-terminus to an amino acid sequence comprising a B-cell

XX epitope of the V3 loop of an HIV env protein, which can be used to

XX generate vaccines against HIV-1. The T-cell epitope sequence is pref.

XX selected from the T-helper determinant core peptides P24E, P24N, P24L,

XX P24M and P24H while the B-cell epitopes are derived from HIV strains

XX including CTLB-56, V2MN, CTLB-29, CTLB-55, SP2, IAI, IIB, RF, 26, 2054,

XX 1714 and BX08. The peptides are chimeric and can be linked to a

XX branched lys backbone. The peptides AAW25853-67 represents chimeric

XX T/B cell epitope peptides which also contain a gp41 neutralisation

SQ Sequence 18 AA;

Query Match

Best Local Similarity 100.0%; Score 48; DB 18; Length 18;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7

Db 11 LMNMFPI 17

Search completed: May 7, 2003, 09:53:53

Job time : 7.38426 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 2.36574 Seconds

(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-5

Perfect score: 48

Sequence: 1 LMNMEDI 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:***
2: PIR1:***
3: PIR3:***
4: PIR4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	357	2	S22006 envelope protein g
2	48	100.0	357	2	S22004 envelope protein g
3	48	100.0	358	2	S21998 envelope protein g
4	48	100.0	843	1	H44001 env polypeptide pr
5	48	100.0	847	2	T09448 envelope glycoprot
6	48	100.0	847	2	S13289 env protein - huma
7	48	100.0	854	1	VCLJSI env polypeptide pr
8	48	100.0	856	1	A44963 env polypeptide pr
9	48	100.0	859	1	VCLJMN env polypeptide pr
10	43	89.6	851	2	S13985 env polypeptide -
11	43	89.6	852	1	VCLJBR env polypeptide -
12	43	89.6	852	2	T12016 envelope glycoprot
13	43	89.6	853	2	S54384 envelope polypept
14	43	89.6	854	2	S13288 env protein - huma
15	43	89.6	855	1	VCLJZR env polypeptide pr
16	43	89.6	856	1	VCLJH3 env polypeptide pr
17	43	89.6	861	1	VCLJLV env polypeptide pr
18	43	89.6	861	1	VCLJSC env polypeptide pr
19	42	87.5	136	2	JU0266 envelope polypept
20	42	87.5	136	2	JU0954 envelope polypept
21	42	87.5	357	2	S21996 envelope polypept
22	42	87.5	357	2	S21992 envelope protein g
23	42	87.5	358	2	S22002 envelope protein g
24	42	87.5	358	2	S22000 envelope protein g
25	42	87.5	358	2	S70417 envelope protein g
26	42	87.5	436	2	G97186 diverged glycosylt
27	42	87.5	443	2	C41621 env polypeptide p
28	42	87.5	454	2	B41621 env polypeptide p
29	42	87.5	729	1	VCLJRX env polypeptide pr

30	42	87.5	846	1	VCLJND env polypeptide pr
31	42	87.5	855	1	VCLJAZ env polypeptide pr
32	42	87.5	856	1	VCLJ3W env polypeptide pr
33	42	87.5	859	2	T01672 envelope polypept
34	42	87.5	861	1	VCLJKB env polypeptide pr
35	42	87.5	1044	2	H97186 glycosyltransferas
36	41	85.4	357	2	S21994 envelope protein g
37	41	85.4	1034	2	G90591 hypothetical prote
38	40	83.3	274	2	E83837 ABC-transporting p
39	40	83.3	606	2	JC5604 probable integral
40	40	83.3	735	2	D86465 gag polypeptide -
41	40	83.3	863	2	A53034 envelope protein p
42	40	83.3	877	2	S49197 dynein heavy chain
43	39	81.2	1114	2	T30299 conserved hypothe
44	39	81.2	1415	2	C83070 probable membrane
45	38	79.2	241	2	S59377

ALIGNMENTS

RESULT 1
S22006
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70420; S22006
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MID:92144209; PMID:1736940
A:Accession: S70420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <SF2>
A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191
A:Experimental source: patient L
A:Note: Submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polypeptide

Query Match 100.0%; Score 48; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMEDI 7
Db 170 LMNMEDI 176
|||||||

RESULT 2
S22004
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22004; S70419
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S22004
A:Molecule type: DNA
A:Residues: 1-357 <SF2>
A:Cross-references: EMBL:X61353; NID:960188; PIDN:CAA43618.1; PID:960189
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MID:92144209; PMID:1736940
A:Accession: S70419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292, 'X', 294-357 <SF2>
A:Cross-references: EMBL:X61353; NID:960188

C:Superfamily: type E retrovirus env polypotein

Query Match

100.0%; Score 48; DB 2; Length 357;

Best Local Similarity

100.0%; Pred. No. 1.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7

DB 170 LMNMFPI 176

RESULT 3

S21998

envelope protein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

A:Variate: isolate 28

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S21998; S70425

R:Stueler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A:Reference number: S21998

A:Accession: S21998

A:Molecule type: DNA

A:Residues: 1-358 <STE1>

A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183

R:Stueler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebri

A:Reference number: S70417; MUID:92144209; PMID:1736940

A:Accession: S70425

A>Status: preliminary

A:Residue type: DNA

A:Residues: 1-222, 'X', 224-358 <STE2>

A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183

C:Superfamily: type E retrovirus env polypotein

Query Match

100.0%; Score 48; DB 2; Length 358;

Best Local Similarity

100.0%; Pred. No. 1.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7

DB 171 LMNMFPI 177

env polypotein precursor - human immunodeficiency virus type 1 (strain YU-2)

N:Alternate names: coat polypotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994

C:Accession: H44001

R:Li, Y.; Hul, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties of

A:Reference number: A44001; MUID:93021387; PMID:1404605

A:Accession: H44001

A:Molecule type: DNA

A:Residues: 1-843 <LIV>

A:Cross-references: GB:M93258

C:Genetics:

C:Superfamily: type E retrovirus env polypotein

C:Keywords: coat protein; glycoprotein; polypotein; transmembrane protein

F:1-39/Domain: signal sequence #status predicted <SIG>

F:19-35/Region: hydrophobic

F:30-489/Product: coat protein gp120 #status predicted <GP1>

F:490-843/Product: coat protein gp41 #status predicted <GP2>

F:499-515/Region: hydrophobic

F:673-688/Region: hydrophobic

F:738-755/Domain: transmembrane #status predicted <TMN>

F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,

Query Match

100.0%; Score 48; DB 1; Length 843;

Best Local Similarity

100.0%; Pred. No. 3.5;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7

DB 656 LMNMFPI 662

RESULT 5

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JRF1)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

C:Accession: T09448

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:91465777; PID:91465781

C:Genetics:

C:Superfamily: type E retrovirus env polypotein

Query Match

100.0%; Score 48; DB 2; Length 847;

Best Local Similarity

100.0%; Pred. No. 3.5;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7

DB 660 LMNMFPI 666

RESULT 6

S13289

env polypotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack,

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13289

A>Status: preliminary

A:Residue type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polypotein

Query Match

100.0%; Score 48; DB 2; Length 847;

Best Local Similarity

100.0%; Pred. No. 3.5;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFPI 7

DB 660 LMNMFPI 666

RESULT 7

VCLJ51

env polypotein precursor - simian immunodeficiency virus SIVcpz

N:Alternate names: coat polypotein

N:Contains: coat protein gp120; coat protein gp41

C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (chimpanzee)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C:Accession: S09990

R:huet, T.; Cheynier, R.; Meyerhans, A.; Koelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:reference number: S09983; MID:90259077; PMID:2188136
A:Accession: S09990
A:status: nucleic acid sequence not shown; translation not shown
A:molecule type: DNA
A:Residues: 1-854 <RUE>
A:Cross-references: EMBL:X52154; NID:958866; PIDN:CAA36407.1; PID:958874
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypro
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-500/Product: coat protein gp120 #status predicted <CP1>
F:501-854/Product: coat protein gp41 #status predicted <CP2>
F:501-517/Domain: transmembrane #status predicted <TM1>
F:675-693/Domain: transmembrane #status predicted <TM2>
F:805-821/Domain: transmembrane #status predicted <TM3>
F:134,140,143,154,158,186,195,239,260,267,274,299,331,336,351,356,384,392,426,432,446,45

Query Match 100.0%; Score 48; DB 1; Length 854;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFEDI 7
|||||
Db 660 LMNMFEDI 666

RESULT 8
A4963
env polyprotein precursor - human immunodeficiency virus type 1 (isolate Z321)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 28-May-1999
C:Accession: A44963
R:Srinivasan, A.; York, D.; Butler Jr., D.; Jannoun-Nasr, R.; Getchell, J.; McCormick, J

AIDS Res. Hum. Retroviruses 5, 121-129, 1989
A:title: Molecular characterization of HIV-1 isolated from a serum collected in 1976: nu
A:reference number: A44963; MID:89228766; PMID:2713163
A:Accession: A44963
A:Molecule type: DNA
A:Residues: 1-856 <SRI>
A:Cross-references: GB:M15896; NID:9329392; PIDN:AAB53948.1; PID:9329394
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-520/Product: coat protein gp120 #status predicted <CP1>
F:521-856/Product: coat protein gp41 #status predicted <CP2>
F:684-705/Domain: transmembrane #status predicted <TM1>
F:87,132,138,152,156,183,198,242,263,277,294,302,393,398,402,411,448,461,462,465,613

Query Match 100.0%; Score 48; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFEDI 7
|||||
Db 669 LMNMFEDI 675

RESULT 9
VCLJMN
env polyprotein precursor - human immunodeficiency virus type 1 (isolate MN)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997

C:Accession: A28922
R:Girgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-
Virology 164, 531-536, 1988
A:title: Envelope sequences of two new United States HIV-1 isolates.
A:reference number: A28922; MID:88219542; PMID:3369091
A:Accession: A28922
A:Molecule type: DNA
A:Residues: 1-859 <CUR>
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane pr
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-859/Product: env polyprotein #status predicted <CP>
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,

Query Match 100.0%; Score 48; DB 1; Length 859;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFEDI 7
|||||
Db 673 LMNMFEDI 679

RESULT 10
S33985
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C:Accession: S33985
R:Carlini, F.
submitted to the EMBL Data Library, November 1991
A:reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: EMBL:Z11530; NID:960192; PIDN:CAA77628.1; PID:960199
C:Superfamily: type E retrovirus env polyprotein

Query Match 89.6%; Score 43; DB 2; Length 851;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFEDI 7
|||||
Db 664 LMNMFEDI 670

RESULT 11
VCLJBR
env polyprotein - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
C:Accession: A31667
R:Andard, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar
Virology 168, 79-89, 1989
A:title: Biological and molecular characterization of human immunodeficiency virus (H
A:reference number: A94389; MID:89085613; PMID:2789516
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: capsid protein; coat protein; polyprotein; transmembrane protein
F:1-516/Product: coat protein gp120 #status predicted <CP1>
F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 89.6%; Score 43; DB 1; Length 852;
Best Local Similarity 85.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMWFDI 7
 |||||:|
 Db 665 LNMWFDI 671

RESULT 12

T12016
 envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T12016
 R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
 AIDS Res. Hum. Retroviruses 14, 329-337, 1998
 A>Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S
 A:Reference number: Z17379; MUID:98178716; PMID:9519894
 A:Accession: T12016
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-852 <MCC>
 A:Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polypotein

Query Match 89.6%; Score 43; DB 2; Length 852;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
 |||||:|
 Db 665 LNMWFDI 671

RESULT 13

S54384
 envelope polypeptide - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999
 C:Accession: S54384
 R:Theodore, T.; Buckler-White, A.J.
 submitted to the EMBL Data Library, July 1989
 A:Reference number: S54377
 A:Accession: S54384
 A:Status: preliminary
 A:Molecule type: genomic RNA
 A:Residues: 1-853 <THE>
 A:Cross-references: EMBL:M26339; NID:g329377; PIDN:AAA5370.1; PID:g329385
 C:Superfamily: type E retrovirus env polypeptide
 C:Keywords: polypeptide

Query Match 89.6%; Score 43; DB 2; Length 853;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
 |||||:|
 Db 666 LNMWFDI 672

RESULT 14

S13288
 env protein - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
 C:Accession: S13288
 R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
 Nature 348, 69-73, 1990
 A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
 A:Reference number: S13288; MUID:91043044; PMID:2172833
 A:Accession: S13288
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-854 <OBR>
 C:Superfamily: type E retrovirus env polypeptide

Query Match 89.6%; Score 43; DB 2; Length 854;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
 |||||:|
 Db 667 LNMWFDI 673

RESULT 15

VCLJ2R
 env polypeptide precursor - human immunodeficiency virus Zr-6
 N:Alternate names: coat polypeptide
 C:Species: human immunodeficiency virus Zr-6
 C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
 C:Accession: D26192
 R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.;
 Gene 52, 71-82, 1987
 A>Title: Molecular characterization of human immunodeficiency virus from Zaire: nucle
 A:Reference number: A26192; MUID:87248097; PMID:3036660
 A:Accession: D26192
 A:Molecule type: DNA
 A:Residues: 1-855 <SRI>
 A:Cross-references: GB:K03458; GB:M16322; NID:g329398; PIDN:AAA5380.1; PID:g329403
 C:Genetics:
 A:Gene: env
 C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-855/Product: env polypeptide #status predicted <MAT>
 F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
 F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
 F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,366,392,398,

Query Match 89.6%; Score 43; DB 1; Length 855;
 Best Local Similarity 85.7%; Pred. No. 22;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
 |||||:|
 Db 668 LNMWFDI 674

Search completed: May 7, 2003, 09:58:39
 Job time : 3.36574 secs

FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 164 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 558 558 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 843 AA: 95648 MW: C69DPD971C918B71 CRC64;

Query Match Similarity 100.0%; Score 48; DB 1; Length 843;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWPI 7
 DB 656 LNMWPI 662

ENV_HV1S1 STANDARD; PRT: 847 AA.

AC P19550; 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90347835; PubMed=2384920;
 RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
 RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
 RL J. Virol. 64:4396-4398(1990).
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CC
 CC EMBL: M65024; AAA45072.1; .
 DR HIV: M38428; ENVSEF162.
 DR InterPro: IPR000328; Env.GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KM AIDS; Coat protein; Glycoprotein; Transmembrane;
 FT SIGNAL 1 29

FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 203 BY SIMILARITY.
 FT DISULFID 125 194 BY SIMILARITY.
 FT DISULFID 130 155 BY SIMILARITY.
 FT DISULFID 216 245 BY SIMILARITY.
 FT DISULFID 226 237 BY SIMILARITY.
 FT DISULFID 294 328 BY SIMILARITY.
 FT DISULFID 374 435 BY SIMILARITY.
 FT DISULFID 381 408 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 847 AA: 96135 MW: 0A901317DF7F2AB CRC64;

Query Match Similarity 100.0%; Score 48; DB 1; Length 847;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWPI 7
 DB 660 LNMWPI 666

ENV_HV1W2 STANDARD; PRT: 847 AA.

AC P05880; 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein Gp160 precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS.";
 RL Science 232:1548-1553(1986).
 CC -1- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

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 CC or send an email to license@isb-sib.ch).

DR EMBL: M12507; AAB12990.1; -
 DR HIV: M12507; ENV5WMD2.
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.

FT	CHAIN	1	29	
FT	CHAIN	30	501	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	502	847	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	202	BY SIMILARITY.
FT	DISULFID	125	193	BY SIMILARITY.
FT	DISULFID	130	152	BY SIMILARITY.
FT	DISULFID	215	244	BY SIMILARITY.
FT	DISULFID	225	236	BY SIMILARITY.
FT	DISULFID	225	326	BY SIMILARITY.
FT	DISULFID	372	435	BY SIMILARITY.
FT	DISULFID	379	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	194	194	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	231	231	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	238	238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	259	259	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	273	273	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	286	286	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	327	327	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	334	334	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	350	350	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	380	380	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	386	386	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	438	438	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	602	602	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	847 AA;	96466 MW;	CDIE33D73AASBDAE CRC64;

Query Match 100.0%; Score 48; DB 1; Length 847;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
 DB 660 LNMWFDI 666

RESULT 4
 ENV_STVCZ STANDARD; PRT; 854 AA.
 AC P17281;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Chimpanzee immunodeficiency virus (SIVcpz) (CIV).
 OC Viruses: Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID:11723;

RP SEQUENCE FROM N.A.
 RA MEDLINE:90259077; PubMed:2188136;
 RA Huet T., Cheyner R., Meyerhans A., Roelants G., Main-Hobson S.;
 RT "Genetic organization of a chimpanzee lentivirus related to HIV-1."
 RU Nature 345:356-359(1990).
 CC -1- SIMILARITY: STRONG, WITH HIV-1 ENV POLYPEPTIDE.

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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).

DR EMBL: X52154; CA36407.1; -
 DR PIR: S09900; VCLJST.
 DR HIV: X52154; ENVSCPZ.
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR Aids: Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.

FT	CHAIN	1	30	
FT	CHAIN	31	500	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	501	854	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	501	517	POTENTIAL.
FT	DISULFID	675	693	POTENTIAL.
FT	DISULFID	805	821	POTENTIAL.
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	143	143	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	267	267	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	351	351	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	426	426	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	446	446	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	601	601	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	608	608	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	854 AA;	95803 MW;	2E249AFADA4F2D9B3 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 854;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
 DB 660 LNMWFDI 666

[illegible]

FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	413	413	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	448	448	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	465	465	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	612	612	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	617	617	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	626	626	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	638	638	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	856 AA;	97140 MW;	D197D809940BE732	CRC64;
Query Match	Best Local Similarity	100.0%;	Score 48;	DB 1;	Length 856;
Matches	7; Conservative	100.0%;	Pred. No. 2.7;	0; Mismatches	0; Indels
0;					Gaps 0;
OY	1 LMNMFID	7			
Db	670.LMNMFID	676			
RESULT 6					
ENV_HV12H	STANDARD;	PRT;	856 AA.		
ID	ENV_HV12H				
AC	P05881;				
DT	01-NOV-1988 (Rel. 09, Created)				
DT	01-NOV-1988 (Rel. 09, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
DE	ENV.				
GN	Human immunodeficiency virus type 1 (Zaire H2321 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae.				
OC	NCBI_TaxID=11692;				
OX	[1]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=89228766; PubMed=2713163;				
RX	Srinivasan A., York D., Butler D. Jr., Jannoun-Nasr R., Getcheil J.,				
RA	McCormick J., Ou C.Y., Myers G., Smith T., Chen E.;				
RA	"Molecular characterization of HIV-1 isolated from a serum collected				
RT	in 1976: nucleotide sequence comparison to recent isolates and				
RT	generation of hybrid HIV."				
RL	AIDS Res. Hum. Retroviruses 5:121-129(1989).				
CC	-----				
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CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M15896; AAB53948.1; -.				
DR	PIR; A44963; A44963.				
DR	HIV; M15896; ENV52321.				
DR	InterPro; IPR000328; ENV_GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120.1.				
DR	Pfam; PF00517; GP41.1.				
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;				
KW	Signal.				
FT	SIGNAL	1	29		
FT	CHAIN	30	511	EXTERIOR MEMBRANE GLYCOPROTEIN.	
FT	CHAIN	512	856	TRANSMEMBRANE GLYCOPROTEIN.	
FT	DISULFID	53	73	BY SIMILARITY.	
FT	DISULFID	118	206	BY SIMILARITY.	
FT	DISULFID	125	197	BY SIMILARITY.	
FT	DISULFID	130	153	BY SIMILARITY.	
FT	DISULFID	219	248	BY SIMILARITY.	
FT	DISULFID	229	240	BY SIMILARITY.	
FT	DISULFID	297	331	BY SIMILARITY.	
FT	DISULFID	379	445	BY SIMILARITY.	

FT DISULFID 386 418 BY SIMILARITY.
 FT CARBOHYD 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 132 132 (POTENTIAL).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 387 387 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 465 465 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 96909 MM; 8396E3FB8BD174E CRC64;

Query Match 100.0%; Score 48; DB 1; Length 856;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
 Db 669 LNMWFDI 675

RESULT 7
 ENV_HV1RH STANDARD; PRT; 865 AA.
 AC P04579;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (RF/RAT isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11701;
 RP MEDLINE=86218077; PubMed=2423250;
 RA Starich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;
 RT Identification and characterization of conserved and variable regions in the envelope gene of HIV-III/LAV, the retrovirus of AIDS.
 RL Cell 45:637-648(1986).
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 CC EMBL: M17451; AAA5057.1;
 DR HIV; M17451; ENVSRF.

DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS: Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
 FT CHAIN 1 29
 FT CHAIN 30 519
 FT CHAIN 520 865
 FT DISULFID 53 73
 FT DISULFID 118 218
 FT DISULFID 125 209
 FT DISULFID 130 157
 FT DISULFID 231 260
 FT DISULFID 241 252
 FT DISULFID 309 343
 FT DISULFID 389 452
 FT DISULFID 396 425
 FT CARBOHYD 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 136 136
 FT CARBOHYD 139 139
 FT CARBOHYD 156 156
 FT CARBOHYD 193 193
 FT CARBOHYD 194 194
 FT CARBOHYD 197 197
 FT CARBOHYD 198 198
 FT CARBOHYD 203 203
 FT CARBOHYD 210 210
 FT CARBOHYD 247 247
 FT CARBOHYD 254 254
 FT CARBOHYD 275 275
 FT CARBOHYD 289 289
 FT CARBOHYD 302 302
 FT CARBOHYD 308 308
 FT CARBOHYD 314 314
 FT CARBOHYD 344 344
 FT CARBOHYD 351 351
 FT CARBOHYD 367 367
 FT CARBOHYD 397 397
 FT CARBOHYD 403 403
 FT CARBOHYD 407 407
 FT CARBOHYD 413 413
 FT CARBOHYD 418 418
 FT CARBOHYD 455 455
 FT CARBOHYD 471 471
 FT CARBOHYD 620 620
 FT CARBOHYD 625 625
 FT CARBOHYD 634 634
 FT CARBOHYD 646 646
 FT CARBOHYD 825 825
 SQ SEQUENCE 865 AA; 97809 MM; 28828BC2314ADCAC CRC64;

Query Match 100.0%; Score 48; DB 1; Length 865;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
 Db 678 LNMWFDI 684

RESULT 8
 FDGX_HAEIN STANDARD; PRT; 1028 AA.
 AC P46448;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Formate dehydrogenase major subunit (PC 1.2.1.2) (formate dehydrogenase alpha subunit) (FDH alpha subunit).
 GN FDGX OR H10006.
 OS Haemophilus influenzae.

FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 89.6%; Score 43; DB 1; Length 851;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
 Db 664 LNMWFDI 670

RESULT 10
 ID ENV_HV1BN STANDARD; PRT; 852 AA.
 AC P12488;
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89085613; PubMed=2789516;
 RA Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.;
 RT "Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia.";
 RT Virology 168:79-89 (1989).
 RL -1- MISCELLANEOUS: THIS VIRUS IS CYTOTOXICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.

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CC EMBL: M21098; AAA44221.1;
 DR PIR: A31667; VCLJBR.
 DR HIV: M21098; ENVSRVA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT CHAIN 1 30
 FT SIGNAL 507
 FT CHAIN 508 852
 FT CHAIN 54 74
 FT DISULFID 119 205
 FT DISULFID 126 156
 FT DISULFID 131 155
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 330
 FT DISULFID 376 439
 FT DISULFID 383 412
 FT CARBOHYD 49 49
 FT CARBOHYD 88 88
 FT CARBOHYD 135 135
 FT CARBOHYD 138 138
 FT CARBOHYD 154 154

EXTERIOR MEMBRANE GLYCOPROTEIN.
 TRANSMEMBRANE GLYCOPROTEIN.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;

Query Match 89.6%; Score 43; DB 1; Length 852;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
 Db 665 LNMWFDI 671

RESULT 11
 ID ENV_HV1BN STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamont C., Mann A.M., Méter C., Wasilak A.;
 RT "Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";
 RT J. Virol. 64:3792-3803 (1990).

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CC EMBL: M33943; AAA44850.1;
 DR HIV: M33943; ENVSRVA.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 397 397
 FT CARBOHYD 406 406
 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 625 625
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA: 97224 MW: 0BFBI18931B27 CRC64;
 Query Match 89.6%; Score 43; DB 1; Length 856;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMWFI 7
 DB 669 LNMWFI 675
 RESULT 15
 ENV_HV1H2 STANDARD; PRT: 856 AA.
 AC P04578; 009779;
 DT 15-AUG-1987 (Rel. 05, Created)
 DT 13-JUL-1999 (Rel. 38, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN Env.
 OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirinae.
 OX NCBI_TaxID=11706;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87299196; PubMed=3040055;
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
 RT "Complete nucleotide sequences of functional clones of the AIDS virus.";
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
 RP REVISIONS.
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,

RA Gallo R.C., Wong-Staal F.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 CC -----
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 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL: K03455; AAB50262.1; -;
 DR EMBL: AF038399; AAB99976.1; -;
 DR EMBL: AF038319; AAC82596.1; -;
 DR HIV: K03455; ENVSHX82.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR pfam: PF00516; GP120.1.
 DR pfam: PF00517; GP41.1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 30
 FT SIGNAL 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 236 331
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 230 230
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
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 FT CARBOHYD 397 397
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 FT CARBOHYD 448 448
 FT CARBOHYD 463 463
 FT CARBOHYD 611 611
 FT CARBOHYD 616 616
 FT CARBOHYD 624 624
 FT CARBOHYD 637 637
 FT CARBOHYD 674 674
 FT CARBOHYD 750 750
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA: 97212 MW: 6FBI6AF85107E0 CRC64;
 Query Match 89.6%; Score 43; DB 1; Length 856;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LNMWFI 7
 DB 669 LNMWFI 675
 EMBL: K03455; AAB50262.1; -;
 EMBL: AF038399; AAB99976.1; -;
 EMBL: AF038319; AAC82596.1; -;
 HIV: K03455; ENVSHX82.
 InterPro: IPR000328; Env_GP41.
 InterPro: IPR000777; GP120.
 pfam: PF00516; GP120.1.
 pfam: PF00517; GP41.1.
 AIDS; Coat protein; Glycoprotein; Transmembrane;
 Signal.
 CHAIN 1 30
 SIGNAL 31 511
 CHAIN 512 856
 DISULFID 54 74
 DISULFID 119 205
 DISULFID 126 196
 DISULFID 131 157
 DISULFID 218 247
 DISULFID 228 239
 DISULFID 236 331
 DISULFID 296 331
 DISULFID 378 445
 DISULFID 385 418
 CARBOHYD 88 88
 CARBOHYD 136 136
 CARBOHYD 141 141
 CARBOHYD 156 156
 CARBOHYD 160 160
 CARBOHYD 186 186
 CARBOHYD 197 197
 CARBOHYD 230 230
 CARBOHYD 241 241
 CARBOHYD 262 262
 CARBOHYD 276 276
 CARBOHYD 289 289
 CARBOHYD 295 295
 CARBOHYD 301 301
 CARBOHYD 332 332
 CARBOHYD 339 339
 CARBOHYD 356 356
 CARBOHYD 386 386
 CARBOHYD 392 392
 CARBOHYD 397 397
 CARBOHYD 406 406
 CARBOHYD 448 448
 CARBOHYD 463 463
 CARBOHYD 611 611
 CARBOHYD 616 616
 CARBOHYD 624 624
 CARBOHYD 637 637
 CARBOHYD 674 674
 CARBOHYD 750 750
 CARBOHYD 816 816
 SEQUENCE 856 AA: 97212 MW: 6FBI6AF85107E0 CRC64;
 Match 89.6%; Score 43; DB 1; Length 856;
 Best Local Similarity 85.7%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Wed May 7 14:34:32 2003

us-09-877-606-5.rsp

Page 11

Search completed: May 7, 2003, 09:54:37
Job time : 2.23148 secs

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 5.02315 Seconds
(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-5
Perfect score: 48
Sequence: 1 LMNMFPI 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	100.0	41	15	069891	069891 human immun
2	48	100.0	41	15	069892	069892 human immun
3	48	100.0	117	15	09YRU0	09YRU0 human immun
4	48	100.0	117	15	09YRT7	09YRT7 human immun
5	48	100.0	117	15	09YRT6	09YRT6 human immun
6	48	100.0	117	15	09WKU0	09WKU0 human immun
7	48	100.0	117	15	09YRT2	09YRT2 human immun
8	48	100.0	117	15	09YRS9	09YRS9 human immun
9	48	100.0	117	15	09YRS1	09YRS1 human immun
10	48	100.0	117	15	09YRS0	09YRS0 human immun
11	48	100.0	117	15	09YRT7	09YRT7 human immun
12	48	100.0	117	15	09QON5	09QON5 human immun
13	48	100.0	118	15	09ES57	09ES57 human immun
14	48	100.0	118	15	09ESR5	09ESR5 human immun
15	48	100.0	118	15	09ESR4	09ESR4 human immun
16	48	100.0	118	15	09ESR3	09ESR3 human immun

17	48	100.0	118	15	09ESR2	09ESR2 human immun
18	48	100.0	118	15	09ESR1	09ESR1 human immun
19	48	100.0	118	15	09ESR0	09ESR0 human immun
20	48	100.0	118	15	09ESQ7	09ESQ7 human immun
21	48	100.0	118	15	09ESQ6	09ESQ6 human immun
22	48	100.0	118	15	09ESQ3	09ESQ3 human immun
23	48	100.0	118	15	09ESQ1	09ESQ1 human immun
24	48	100.0	118	15	09ESQ8	09ESQ8 human immun
25	48	100.0	118	15	09ESQ6	09ESQ6 human immun
26	48	100.0	119	15	09IHU5	09IHU5 human immun
27	48	100.0	119	15	09TR05	09TR05 human immun
28	48	100.0	121	15	09ODJ5	09ODJ5 human immun
29	48	100.0	121	15	09UR98	09UR98 human immun
30	48	100.0	121	15	08UR03	08UR03 human immun
31	48	100.0	121	15	08UCW7	08UCW7 human immun
32	48	100.0	122	15	09YXR7	09YXR7 human immun
33	48	100.0	122	15	09YXR2	09YXR2 human immun
34	48	100.0	122	15	09YXR1	09YXR1 human immun
35	48	100.0	122	15	09YXR0	09YXR0 human immun
36	48	100.0	122	15	09YXQ9	09YXQ9 human immun
37	48	100.0	122	15	09YXQ7	09YXQ7 human immun
38	48	100.0	122	15	09YXQ5	09YXQ5 human immun
39	48	100.0	122	15	09YXQ4	09YXQ4 human immun
40	48	100.0	122	15	09YXQ3	09YXQ3 human immun
41	48	100.0	122	15	09YXQ1	09YXQ1 human immun
42	48	100.0	122	15	09YXQ0	09YXQ0 human immun
43	48	100.0	122	15	09YXP8	09YXP8 human immun
44	48	100.0	122	15	09YXP7	09YXP7 human immun
45	48	100.0	122	15	09YXP5	09YXP5 human immun

ALIGNMENTS

RESULT 1
ID 069891 PRELIMINARY; PRT; 41 AA.
AC 069891;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emml E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by TM-41-25, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06721; AAA19134.1; -
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 41 41
SQ SEQUENCE 41 AA; 5082 MW; 089C7E2CDD403CC6 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 41;
Best local similarity 100.0%; Pred. No. 0.7; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Oy 1 LMNMFPI 7
Db 30 LMNMFPI 36

RESULT 2

069892
ID 069892 PRELIMINARY; PRT; 41 AA.
AC 069892;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GP41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by 1A4-41-2F5, an anti-GP41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; 006722; AAA19135.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 41
SQ SEQUENCE 41 AA; 5081 MW; DB9C70CC3403CC6 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWEDI 7
DB 30 LMNWEDI 36

RESULT 3
OYRU0 PRELIMINARY; PRT; 117 AA.

ID 09YRU0
AC 09YRU0;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96USNG570;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storch C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF096325; AAD04400.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13941 MW; F26E40AD3DFB1B60 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWEDI 7
DB 109 LMNWEDI 115

RESULT 4
OYRT7 PRELIMINARY; PRT; 117 AA.
AC 09YRT7;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96USNG17;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storch C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF096328; AAD04403.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13985 MW; 959F54B7B3F7E9E CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWEDI 7
DB 109 LMNWEDI 115

RESULT 5
OYRT6 PRELIMINARY; PRT; 117 AA.
AC 09YRT6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=96USNG58;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storch C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RT Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF096329; AAD04404.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13962 MW; 83A17E3F6154966C CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWEDI 7
|||||
Db 109 LMNWEDI 115

RESULT 6

Q9WKU0 PRELIMINARY; PRT; 117 AA.
AC Q9WKU0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG15;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M., Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C., Jones J., Ward J.;
RT Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096333; AAD04408.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KM Transmembrane.
FT NON_TER 1
FT 117
SQ SEQUENCE 117 AA; 13959 MW; BBA0CA6FDE179BEC CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 LMNWEDI 7
|||||
Db 109 LMNWEDI 115

RESULT 7
Q9YRT2 PRELIMINARY; PRT; 117 AA.
AC Q9YRT2;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USNG15;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M., Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C., Jones J., Ward J.;
RT Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096334; AAD04409.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KM Transmembrane.
FT NON_TER 1
FT 117
SQ SEQUENCE 117 AA; 13959 MW; DED23BB02B524D9 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;

Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWEDI 7
|||||
Db 109 LMNWEDI 115

RESULT 8

Q9YRS9 PRELIMINARY; PRT; 117 AA.
AC Q9YRS9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USN94;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M., Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C., Jones J., Ward J.;
RT Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096337; AAD04412.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KM Transmembrane.
FT NON_TER 1
FT 117
SQ SEQUENCE 117 AA; 13953 MW; F1A817AD1A50B77B CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.9; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 LMNWEDI 7
|||||
Db 109 LMNWEDI 115

RESULT 9
Q9YRS1 PRELIMINARY; PRT; 117 AA.
AC Q9YRS1;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USCF72;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M., Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C., Jones J., Ward J.;
RT Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096345; AAD04420.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KM Transmembrane.
FT NON_TER 1
FT 117
SQ SEQUENCE 117 AA; 13953 MW; F1A817AD1A50B77B CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;

SO SEQUENCE 117 AA; 13925 MW; 09DF32E239BD59D0 CRC64;
Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 117;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMEDI 7
117
DB 109 LMNMEDI 115
RESULT 10
QYRSO PRELIMINARY; PRT; 117 AA.
AC QYRSO;
DT 01-MAY-1999 (TREMELREL. 10, Created)
DT 01-MAY-1999 (TREMELREL. 10, last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97USC31;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096346; AAD04421.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KM Transmembrane.
FT NON_TER 1
KW 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 14006 MW; 7440C1BA73F95719 CRC64;
Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 117;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMEDI 7
117
DB 109 LMNMEDI 115
RESULT 11
QYRR7 PRELIMINARY; PRT; 117 AA.
AC QYRR7;
DT 01-MAY-1999 (TREMELREL. 10, Created)
DT 01-MAY-1999 (TREMELREL. 10, last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97USNG30;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF096349; AAD04424.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.

KW Transmembrane.
FT NON_TER 1
KW 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 14003 MW; 8C093B8E9365BCEP CRC64;
Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 117;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMEDI 7
117
DB 109 LMNMEDI 115
RESULT 12
QYQON5 PRELIMINARY; PRT; 117 AA.
AC QYQON5;
DT 01-MAY-2000 (TREMELREL. 13, Created)
DT 01-MAY-2000 (TREMELREL. 13, last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, last annotation update)
DE Envelope glycoprotein gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96USHRP57;
RA Ellenberger D., Sullivan P.S., Dorn J., Schable C., Spira T.J.,
RA Folks T.M., Lal R.B.;
RT "Viral and Immunologic Examination of HIV-1-Infected Persistently
RT Seronegative (HIV) Persons.";
RL J. Infect. Dis. 0:0-0(1999).
DR EMBL: AF157468; AAD45886.1; -
DR InterPro: IPR000328; Env_Gp41.
DR Pfam: PF00517; Gp41; 1.
KM Transmembrane.
FT NON_TER 1
KW 117
FT NON_TER 117
SQ SEQUENCE 117 AA; 14011 MW; 9A71687C21470E60 CRC64;
Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 117;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMEDI 7
117
DB 109 LMNMEDI 115
RESULT 13
QYESS7 PRELIMINARY; PRT; 118 AA.
AC QYESS7;
DT 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA4102;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon.";
RL Aids Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN-CAM102;
RA Fonjungo P.N., Mpoudi E.N., Torimiro J.N., Alemuji G.A., Eno L.T.,
RA Nengasong J.N., Gao F., Rayfield M., Folks T.M., Pleniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252094; AAG14303.1; -
DR InterPro; IPR000328; Env_GPA1.
DR Pfam; PF00517; GPA1; 1.
KW Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 118 AA; 14289 MW; A4987BBE4382CF9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 118;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWNMFDT 7
DB 105 LWNMFDT 111

RESULT 14
Q9E5R5 PRELIMINARY; PRT; 118 AA.
AC Q9E5R5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID-11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM167;
RX MEDLINE-20414627; PubMed-10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM167;
RA Fonjungo P.N., Mpoudi E.N., Torimiro J.N., Alemuji G.A., Eno L.T.,
RA Nengasong J.N., Gao F., Rayfield M., Folks T.M., Pleniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252106; AAG14315.1; -
DR InterPro; IPR000328; Env_GPA1.
DR Pfam; PF00517; GPA1; 1.
KW Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 118 AA; 14175 MW; DBF7416D08ADC38C CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 118;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWNMFDT 7
DB 105 LWNMFDT 111

RESULT 15
Q9E5R4 PRELIMINARY; PRT; 118 AA.
AC Q9E5R4;
DT 01-MAR-2001 (TReMBLrel. 16, Created)

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DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID-11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM170;
RX MEDLINE-20414627; PubMed-10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM170;
RA Fonjungo P.N., Mpoudi E.N., Torimiro J.N., Alemuji G.A., Eno L.T.,
RA Nengasong J.N., Gao F., Rayfield M., Folks T.M., Pleniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252107; AAG14316.1; -
DR InterPro; IPR000328; Env_GPA1.
DR Pfam; PF00517; GPA1; 1.
KW Transmembrane.
FT NON_TER 1 1
SQ SEQUENCE 118 AA; 14188 MW; 34BAEFF75BC91CC8 CRC64;

Query Match
Best Local Similarity 100.0%; Score 48; DB 15; Length 118;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWNMFDT 7
DB 105 LWNMFDT 111

Search completed: May 7, 2003, 09:57:20
Job time : 6.02315 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 2.07407 Seconds
(without alignments)
99.302 Million cell updates/sec

Title: US-09-877-606-5

Perfect score: 48
Sequence: 1 LNMWFDI 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	15	1	US-08-257-528B-59
2	48	100.0	15	1	US-08-460-602A-59
3	48	100.0	15	1	US-08-463-966A-59
4	48	100.0	15	1	US-08-465-217A-59
5	48	100.0	15	2	US-08-464-329A-59
6	48	100.0	15	2	US-08-462-507A-59
7	48	100.0	15	2	US-08-467-881A-59
8	48	100.0	18	1	US-08-257-528B-57
9	48	100.0	18	1	US-08-460-602A-57
10	48	100.0	18	1	US-08-463-966A-57
11	48	100.0	18	1	US-08-465-217A-57
12	48	100.0	18	2	US-08-464-329A-57
13	48	100.0	18	2	US-08-462-507A-57
14	48	100.0	18	2	US-08-467-881A-57
15	48	100.0	20	1	US-08-218-025A-86
16	48	100.0	20	1	US-08-257-528B-86
17	48	100.0	20	1	US-08-460-602A-86
18	48	100.0	20	1	US-08-463-966A-86
19	48	100.0	20	1	US-08-465-217A-86
20	48	100.0	20	2	US-08-464-329A-86
21	48	100.0	20	2	US-08-462-507A-86
22	48	100.0	20	2	US-08-467-881A-86
23	48	100.0	30	1	US-08-257-528B-55
24	48	100.0	30	1	US-08-460-602A-55
25	48	100.0	30	1	US-08-463-966A-55
26	48	100.0	30	1	US-08-465-217A-55
27	48	100.0	30	2	US-08-464-329A-55

28	48	100.0	30	2	US-08-462-507A-58	Sequence 58, Appl
29	48	100.0	30	2	US-08-467-881A-58	Sequence 58, Appl
30	48	100.0	33	1	US-08-257-528B-56	Sequence 56, Appl
31	48	100.0	33	1	US-08-460-602A-56	Sequence 56, Appl
32	48	100.0	33	1	US-08-463-966A-56	Sequence 56, Appl
33	48	100.0	33	1	US-08-465-217A-56	Sequence 56, Appl
34	48	100.0	33	2	US-08-464-329A-56	Sequence 56, Appl
35	48	100.0	33	2	US-08-462-507A-56	Sequence 56, Appl
36	48	100.0	33	2	US-08-467-881A-56	Sequence 56, Appl
37	48	100.0	35	1	US-08-257-528B-54	Sequence 54, Appl
38	48	100.0	35	1	US-08-460-602A-54	Sequence 54, Appl
39	48	100.0	35	1	US-08-463-966A-54	Sequence 54, Appl
40	48	100.0	35	1	US-08-465-217A-54	Sequence 54, Appl
41	48	100.0	35	2	US-08-464-329A-54	Sequence 54, Appl
42	48	100.0	35	2	US-08-462-507A-54	Sequence 54, Appl
43	48	100.0	35	2	US-08-467-881A-54	Sequence 54, Appl
44	48	100.0	138	4	US-09-570-921-18	Sequence 8, Appl
45	48	100.0	138	4	US-09-570-921-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-257-528B-59
; Sequence 59, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: STA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS-Jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-257-528B-59

Query Match 100.0%; Score 48; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI.7
DB 8 LNMWFDI 14

RESULT 2
US-08-460-602A-59
Sequence 59, Application US/08460602A
Patent No. 5759769
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIm & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,602A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-59

Query Match 100.0%; Score 48; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 7; Conservative 0; Mismatches .0; Indels 0; Gaps 0;

OY 1 LMWPMFI 7
DB 8 LMWPMFI 14

RESULT 3
US-08-463-966A-59
Sequence 59, Application US/08463966A
Patent No. 5793955
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIm & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario

COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-59

Query Match 100.0%; Score 48; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMWPMFI 7
DB 8 LMWPMFI 14

RESULT 4
US-08-465-217A-59
Sequence 59, Application US/08465217A
Patent No. 5808822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIm & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-59

Query Match 100.0%; Score 48; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMWPMI 7
| | | | |
DB 8 LMWPMI 14

RESULT 5
US-08-464-329A-59
Sequence 59, Application US/08464329A
Patent No. 5817/54
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-59

Query Match 100.0%; Score 48; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMWPMI 7
| | | | |
DB 8 LMWPMI 14

RESULT 6
US-08-462-507A-59
Sequence 59, Application US/08462507A
Patent No. 5876/31
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-59

Query Match 100.0%; Score 48; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMWPMI 7
| | | | |
DB 8 LMWPMI 14

RESULT 7
US-08-467-881A-59

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; Sequence 59, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-881A-59
;
; Query Match 100.0%; Score 48; DB 2; Length 15;
; Best Local Similarity 100.0%; Pred. NO. 0.047;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LMNMFDI 7
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DB 8 LMNMFDI 14
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RESULT 8
US-08-257-528B-57
; Sequence 57, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-257-528B-57
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QY 1 LMNMFDI 7
    |||||
DB 11 LMNMFDI 17

; Query Match 100.0%; Score 48; DB 1; Length 18;
; Best Local Similarity 100.0%; Pred. NO. 0.057;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 9
US-08-460-602A-57
; Sequence 57, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,602A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
```


TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-57

Query Match 100.0%; Score 48; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
|||||||
Db 11 LNMWFDI 17

RESULT 10
US-08-463-966A-57
Sequence 57, Application US/08463966A
Patent No. 5795955
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-57

Query Match 100.0%; Score 48; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
|||||||

Db 11 LNMWFDI 17

RESULT 11
US-08-465-217A-57
Sequence 57, Application US/08465217A
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-57

Query Match 100.0%; Score 48; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
|||||||
Db 11 LNMWFDI 17

RESULT 12
US-08-464-329A-57
Sequence 57, Application US/08464329A
Patent No. 5817754
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney

STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-57

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFDI 7
DB 11 LMNWFDI 17

RESULT 13
US-08-462-507A-57
Sequence 57, Application US/08462507A
Patent No. 5876731
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-57

Query Match 100.0%; Score 48; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFDI 7
DB 11 LMNWFDI 17

RESULT 14
US-08-467-881A-57
Sequence 57, Application US/08467881A
Patent No. 5951986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-57

Query Match 100.0%; Score 48; DB 2; Length 18;
Best local Similarity 100.0%; Pred. No. 0.057;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWNWFDI 7
Db 11 LWNWFDI 17

RESULT 15

US-08-218-025A-86
Sequence 86, Application US/08218025A
Patent No. 5556744
GENERAL INFORMATION:
APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: P.O. Box 457, 321 No. 5556744istown Road
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST33A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ. ID NO.: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-218-025A-86

Query Match 100.0%; Score 48; DB 1; Length 20;
Best local Similarity 100.0%; Pred. No. 0.064;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWNWFDI 7
Db 10 LWNWFDI 16

Search completed: May 7, 2003, 09:59:50
Job time: 3.07407 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 3.85648 Seconds

(without alignments)
167,038 Million cell updates/sec

Title: US-09-877-606-5

Perfect score: 48

Sequence: 1 LMNMFDI 7

Scoring table: BIOSUM62

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Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	48	100.0	267	10	US-09-854-816-15
3	48	100.0	268	10	US-09-854-816-8
4	48	100.0	268	10	US-09-854-816-13
5	48	100.0	268	10	US-09-854-816-14
6	48	100.0	268	10	US-09-854-816-26
7	48	100.0	268	10	US-09-854-816-35
8	48	100.0	268	10	US-09-854-816-39
9	48	100.0	268	10	US-09-854-816-40
10	48	100.0	268	10	US-09-854-816-68
11	48	100.0	268	10	US-09-854-816-70
12	48	100.0	268	10	US-09-854-816-71
13	48	100.0	269	10	US-09-854-816-72
14	48	100.0	269	10	US-09-854-816-20
15	48	100.0	269	10	US-09-854-816-21
16	48	100.0	269	10	US-09-854-816-22
17	48	100.0	269	10	US-09-854-816-33
18	48	100.0	269	10	US-09-854-816-34
19	48	100.0	269	10	US-09-854-816-37

20	48	100.0	269	10	US-09-854-816-96	Sequence 96, Appl
21	48	100.0	270	10	US-09-854-816-67	Sequence 67, Appl
22	48	100.0	351	9	US-09-886-156-46	Sequence 46, Appl
23	48	100.0	351	9	US-09-886-150-46	Sequence 46, Appl
24	48	100.0	351	9	US-09-886-149-46	Sequence 46, Appl
25	48	100.0	351	9	US-09-886-159-46	Sequence 46, Appl
26	48	100.0	579	9	US-10-032-162-15	Sequence 15, Appl
27	48	100.0	619	10	US-09-891-609-4	Sequence 4, Appl
28	48	100.0	625	9	US-10-032-162-17	Sequence 17, Appl
29	48	100.0	643	9	US-10-032-162-13	Sequence 13, Appl
30	48	100.0	646	10	US-09-891-609-2	Sequence 2, Appl
31	48	100.0	847	10	US-09-476-242-2	Sequence 2, Appl
32	44	91.7	269	10	US-09-854-816-42	Sequence 42, Appl
33	43	89.6	56	10	US-09-779-161-4	Sequence 4, Appl
34	43	89.6	177	9	US-10-040-3498-2	Sequence 2, Appl
35	43	89.6	221	9	US-10-059-271-84	Sequence 84, Appl
36	43	89.6	232	9	US-10-059-271-81	Sequence 81, Appl
37	43	89.6	243	10	US-09-854-816-73	Sequence 73, Appl
38	43	89.6	254	9	US-10-059-271-82	Sequence 82, Appl
39	43	89.6	256	9	US-10-059-271-97	Sequence 97, Appl
40	43	89.6	268	10	US-09-854-816-9	Sequence 9, Appl
41	43	89.6	268	10	US-09-854-816-10	Sequence 10, Appl
42	43	89.6	268	10	US-09-854-816-16	Sequence 16, Appl
43	43	89.6	268	10	US-09-854-816-17	Sequence 17, Appl
44	43	89.6	268	10	US-09-854-816-18	Sequence 18, Appl
45	43	89.6	268	10	US-09-854-816-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-000-321-10
Sequence 10, Application US/10000321
Patent No. US20020123039A1

GENERAL INFORMATION:
APPLICANT: BRUST, Stefan
KNAPP, Stefan
GERKEN, Manfred
GUERTLER, Lutz
TITLE OF INVENTION: Peptides derived from a retrovirus of the HIV group, and their use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/000,321
FILING DATE: 04-Dec-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/131,551
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 58315/106/BEAK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids

TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-000-321-10

Query Match 100.0%; Score 48; DB 12; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
|||||||
DB 138 LNMWFDI 144

RESULT 2
US-09-854-816-15
Sequence 15, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-854-816-15

Query Match 100.0%; Score 48; DB 10; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
|||||||
DB 198 LNMWFDI 204

RESULT 3

US-09-854-816-8
Sequence 8, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-854-816-8

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
|||||||
DB 199 LNMWFDI 205

RESULT 4
US-09-854-816-13
Sequence 13, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-854-816-13

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
DB 199 LNMWFDI 205

RESULT 5
US-09-854-816-14
Sequence 14, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-854-816-14

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFDI 7
DB 199 LNMWFDI 205

RESULT 6
US-09-854-816-26
Sequence 26, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatlin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-854-816-26

Query Match 100.0%; Score 48; DB 10; Length 268;

Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
|||||||
DB 199 LNMWFDI 205

RESULT 7

US-09-854-816-35
Sequence 35, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik

JAMES A. WELLS

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-09-854-816-35

Query Match 100.0%; Score 48; DB 10; Length 268;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
|||||||
DB 199 LNMWFDI 205

RESULT 8

US-09-854-816-39
Sequence 39, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice
Robert S. McDowell

J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: P1005R2

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-854-816-39

Query Match 100.0%; Score 48; DB 10; Length 268;

Best Local Similarity 100.0%; Pred. No. 4.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWFDI 7
|||||||
DB 199 LNMWFDI 205

RESULT 9

US-09-854-816-40
Sequence 40, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik

JAMES A. WELLS

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-854-816-40
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
QY 1 LMNMFEDI 7
Db 199 LMNMFEDI 205
RESULT 10
US-09-854-816-68
Sequence 68, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-854-816-68
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
QY 1 LMNMFEDI 7
Db 199 LMNMFEDI 205
RESULT 11
US-09-854-816-70
Sequence 70, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-854-816-70
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;
QY 1 LMNMFEDI 7
Db 199 LMNMFEDI 205

RESULT 12
US-09-854-816-71
Sequence 71, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasilk
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 71:
US-09-854-816-71
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMFID 7
DB 199 LMNMFID 205
RESULT 13
US-09-854-816-72
Sequence 72, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasilk
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-09-854-816-72
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMFID 7
DB 199 LMNMFID 205
RESULT 14
US-09-854-816-20
Sequence 20, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasilk
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-854-816-20
SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Query Match 100.0%; Score 48; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNNWFDI 7
|||||||
Db 200 LNNWFDI 206

RESULT 15
US-09-854-816-21
Sequence 21, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-854-816-21
SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Query Match 100.0%; Score 48; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNNWFDI 7
|||||||
Db 200 LNNWFDI 206

Search completed: May 7, 2003, 10:21:54
Job time: 3.85648 secs

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:40:21 ; Search time 5.47222 Seconds
(without alignments)
146.102 Million cell updates/sec

Title: US-09-877-606-6
Perfect score: 35
Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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14: /SID2/gcgdata/geneseq/genesep-emb1/AA1993.DAT:*
15: /SID2/gcgdata/geneseq/genesep-emb1/AA1994.DAT:*
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23: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	35	100.0	6	14 AAR43703	HIV-1 gp160 epitope
2	35	100.0	6	16 AAR68698	Katlinger's neutral
3	35	100.0	6	17 AAR92010	HIV-1 gp41 epitope
4	35	100.0	6	18 AAM25868	HIV-1 gp41 epitope
5	35	100.0	6	19 AAM67384	Katlinger's neutral
6	35	100.0	6	19 AAM53143	HIV gp41-contained
7	35	100.0	6	20 AAY39717	HIV1 chimeric pep
8	35	100.0	6	20 AAM99905	HIV-1 vaccine synt
9	35	100.0	6	21 AAB24104	HIV-1 gp41 epitope
10	35	100.0	6	21 AAY57748	Peptide amino acid

11	35	100.0	6	22 AAG63974	Amino acid sequenc
12	35	100.0 <td>6</td> <td>22 AAG63933</td> <td>Amino acid sequenc</td>	6	22 AAG63933	Amino acid sequenc
13	35	100.0 <td>6</td> <td>22 AAB98918</td> <td>HIV epitope ELDKWA</td>	6	22 AAB98918	HIV epitope ELDKWA
14	35	100.0 <td>6</td> <td>22 AAB92333</td> <td>Virus related pep</td>	6	22 AAB92333	Virus related pep
15	35	100.0 <td>6</td> <td>22 AAG65282</td> <td>HIV-1 isolate BH10</td>	6	22 AAG65282	HIV-1 isolate BH10
16	35	100.0 <td>6</td> <td>23 AAO14868</td> <td>HIV epitope peptid</td>	6	23 AAO14868	HIV epitope peptid
17	35	100.0 <td>6</td> <td>23 AAB07403</td> <td>HIV-1 gp41 epitope</td>	6	23 AAB07403	HIV-1 gp41 epitope
18	35	100.0 <td>7</td> <td>16 AAR71631</td> <td>HIV-1 gp41 epitope</td>	7	16 AAR71631	HIV-1 gp41 epitope
19	35	100.0 <td>7</td> <td>17 AAR94444</td> <td>HIV-1 gp41 B-cell</td>	7	17 AAR94444	HIV-1 gp41 B-cell
20	35	100.0 <td>7</td> <td>18 AAM25897</td> <td>Peptide containing</td>	7	18 AAM25897	Peptide containing
21	35	100.0 <td>7</td> <td>19 AAM67413</td> <td>HIV-1 gp41 protein</td>	7	19 AAM67413	HIV-1 gp41 protein
22	35	100.0 <td>7</td> <td>20 AAY39741</td> <td>HIV1 chimeric pep</td>	7	20 AAY39741	HIV1 chimeric pep
23	35	100.0 <td>7</td> <td>20 AAM99911</td> <td>HIV-1 vaccine synt</td>	7	20 AAM99911	HIV-1 vaccine synt
24	35	100.0 <td>7</td> <td>21 AAM29401</td> <td>HIV-1 envelope pro</td>	7	21 AAM29401	HIV-1 envelope pro
25	35	100.0 <td>7</td> <td>22 AAM70190</td> <td>P3 peptide linear</td>	7	22 AAM70190	P3 peptide linear
26	35	100.0 <td>7</td> <td>22 AAG63975</td> <td>Amino acid sequenc</td>	7	22 AAG63975	Amino acid sequenc
27	35	100.0 <td>7</td> <td>22 AAM97480</td> <td>HIV-1 infection in</td>	7	22 AAM97480	HIV-1 infection in
28	35	100.0 <td>7</td> <td>23 AAO80301</td> <td>HIV-1 canonical ep</td>	7	23 AAO80301	HIV-1 canonical ep
29	35	100.0 <td>8</td> <td>16 AAR71632</td> <td>MN-HIV gp41 fragme</td>	8	16 AAR71632	MN-HIV gp41 fragme
30	35	100.0 <td>8</td> <td>20 AAY05254</td> <td>HIV A02 super moti</td>	8	20 AAY05254	HIV A02 super moti
31	35	100.0 <td>8</td> <td>22 AAB12063</td> <td>HIV A02 super moti</td>	8	22 AAB12063	HIV A02 super moti
32	35	100.0 <td>8</td> <td>22 AAB12065</td> <td>HIV A02 super moti</td>	8	22 AAB12065	HIV A02 super moti
33	35	100.0 <td>8</td> <td>22 AAB15180</td> <td>HIV A02 super moti</td>	8	22 AAB15180	HIV A02 super moti
34	35	100.0 <td>8</td> <td>22 AAB20177</td> <td>HIV A03 super moti</td>	8	22 AAB20177	HIV A03 super moti
35	35	100.0 <td>8</td> <td>23 AAO97481</td> <td>HIV A03 motif env</td>	8	23 AAO97481	HIV A03 motif env
36	35	100.0 <td>9</td> <td>16 AAR71637</td> <td>HIV-1 infection in</td>	9	16 AAR71637	HIV-1 infection in
37	35	100.0 <td>9</td> <td>20 AAM99914</td> <td>Immunization contr</td>	9	20 AAM99914	Immunization contr
38	35	100.0 <td>9</td> <td>22 AAB12211</td> <td>HIV A02 super moti</td>	9	22 AAB12211	HIV A02 super moti
39	35	100.0 <td>9</td> <td>22 AAB15290</td> <td>HIV A02 super moti</td>	9	22 AAB15290	HIV A02 super moti
40	35	100.0 <td>9</td> <td>22 AAB18573</td> <td>HIV B62 super moti</td>	9	22 AAB18573	HIV B62 super moti
41	35	100.0 <td>9</td> <td>22 AAB20096</td> <td>HIV A03 motif env</td>	9	22 AAB20096	HIV A03 motif env
42	35	100.0 <td>10</td> <td>21 AAB38721</td> <td>HIV-1 peptide epit</td>	10	21 AAB38721	HIV-1 peptide epit
43	35	100.0 <td>10</td> <td>21 AAB38722</td> <td>HIV-1 peptide epit</td>	10	21 AAB38722	HIV-1 peptide epit
44	35	100.0 <td>10</td> <td>21 AAB38723</td> <td>HIV-1 peptide epit</td>	10	21 AAB38723	HIV-1 peptide epit
45	35	100.0 <td>10</td> <td>22 AAB11616</td> <td>HIV A01 super moti</td>	10	22 AAB11616	HIV A01 super moti

ALIGNMENTS

RESULT 1
AAR43703
ID AAR43703 standard; Peptide; 6 AA.
AC AAR43703;
XX
DT 10-AUG-1995 (first entry)
XX
DE HIV-1 gp160 epitope, residues 662-667, from isolate BH10.
XX
KM Epitope; gp160; strain; isolate; HIV-1; antibody; monoclonal antibody;
XX 2F5; vaccine.
OS Human immunodeficiency virus type 1.
XX
PN EP570357-A.
XX
PD 18-NOV-1993.
XX
PE 13-MAY-1993; 93EP-0890100.
XX
PR 14-MAY-1992; 92AT-0000987.
PR 29-AUG-1992; 92US-0932787.
XX
PA (KAT1/) KATINGER H.
XX
XX Himmler G, Katlinger H, Malwald G, Muster T, Puttscher M;
PI Rucker F, Steindl F, Trkola A, Rucker F;
XX
DR WPI: 1993-361543/46.
DR N-PSDB; AAO51572.
XX
PT Peptides that induce antibodies which neutralise genetically

PT divergent HIV-1 isolates - used as recombinant fusion proteins,
PT recombinant chimeric vaccines or recombinant antibodies
XX
XX Claim 1; Page 7; 41pp; English.
PS
CC The sequences given in AA051572-96 encode epitopes of gp160 derived
CC from different strains and isolates of HIV-1. The peptides encoded
CC by these sequences induce antibodies which neutralise genetically
CC divergent HIV-1 isolates. They bind specifically to the monoclonal
CC antibody 2F5. The peptides comprise just 6 amino acids derived from
CC the gp160 and represent highly conserved epitopes which means that
CC antibodies raised against them will be active against a variety of
CC HIV-1 isolates. The peptides can be used as recombinant fusion
CC proteins, recombinant chimeric vaccines or as recombinant antibodies.
CC They may also be used to link the variable domains of a single
CC chain Fv fragment, or to substitute one or more parts of a Mab peptide
CC sequence.
CC
CC Sequence 6 AA;
SO

Query Match 100.0%; Score 35; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 2
AAR68698
ID AAR68698 standard; peptide; 6 AA.
XX
XX AAR68698;
AC
XX
DT 07-SEP-1995 (first entry)
XX
DE Katlinger's neutralisation epitope.
XX
XX T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen;
KW gp160; gag; pol; vaccine; multimeric peptide; AIDS; 3D organisation.
RV
XX
OS Human immunodeficiency virus type 1.
XX
XX W09429339-A.
PN
PD 22-DEC-1994.
XX
PF 08-JUN-1994; 94WO-CA00317.
XX
PR 09-JUN-1993; 93US-0073378.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XI
II Chong P, Klein MH, Sia CDY;
DR WPI: 1995-036400/05.
XX
XX
XX

Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell
epitope of gag protein linked to B-cell epitope of V3 loop
protein of an HIV-I isolate

Claim 4; Page 16; 69pp; English.

This sequence represents a B-cell epitope, which represents the
gp160 derived epitope, Katlinger's neutralising epitope. This
peptide and other peptides containing this sequence may be linked to
T-cell epitopes, eg. T1 or p24E to form a chimeric protein. This
chimeric peptide is recognised by monoclonal antibody 2F5. Chimeric
peptides such as this, may be used in the production of HIV-1 vaccines.
These peptide sequences may also be used in the production of
multimeric peptides in which the peptides are C-terminally modified by
the addition of a Lys residue which is modified on its epsilon amino

```

CC      acid to carry an additional copy of the peptide molecule. The linear
CC      and multimeric peptides may be used for the treatment of AIDS by acting
CC      to displace the binding of HIV virus to human or animal cells or by
CC      disturbing the 3D organisation of the virus.
CC      xx
SQ      Sequence      6 AA;

Query Match      100.0%; Score 35; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.Be+05;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0.

OY      1 ELDKWA 6
        |||||
Db       1 ELDKWA 6

RESULT 3
AAR92010
ID      AAR92010 standard; Protein; 6 AA.
XX
XX      AAR92010;
XX
XX      27-SEP-1996 (first entry)
XX
XX      HIV-1 gp41 epitope, for insertion in Mycobacterium alpha antigen.
XX
XX      Mycobacterium bovis BCG; AIDS vaccine; surface protein;
XX      alpha antigen; Human immunodeficiency virus type 1; fusion protein;
XX      gp41 epitope.
XX
XX      Human immunodeficiency virus type 1.
XX      OS
XX      WO9604009-A1.
XX      FN
XX      15-FEB-1996.
XX      PD
XX      31-JUL-1995; 95WO-JP01515.
XX      PE
XX      29-JUL-1994; 94JP-0178462.
XX      PR
XX
XX      (AJIN ) AJINOMOTO CO INC.
XX      PA      (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX      XX
XX      Chujo Y, Honda M, Matsuo K, Tasaka H, Yamazaki A;
XX      PI      Yamazaki S;
XX      P1
XX      WPI: 1996-129127/13.
XX      DR      N-PSDB; AAT16054.
XX
XX      BCG containing vaccine secretes chimeric protein containing foreign
XX      PT      antigen - has enhanced immunogenicity and antigenicity esp. when
XX      PT      used as an anti-AIDS vaccine
XX
XX      Example 14; Page 29; 56pp; Japanese.
XX      PS
XX
XX      Antigenic peptides can be inserted into the alpha-antigen sequence
XX      CC      of a Mycobacterium and secreted from an appropriately transformed
XX      CC      M.bovis BCG cell. The resulting chimeric antigen has greatly
XX      CC      enhanced antigenicity and immunogenicity and is recognised in vivo
XX      CC      by B-cells which recognise the alpha-antigen. The present sequence
XX      CC      is that of a HIV-1 gp41 loop epitope which was incorporated
XX      CC      into the alpha antigen. M.bovis BCG cells secreting a
XX      CC      chimeric protein comprising the epitope sequence are useful as
XX      CC      anti-AIDS vaccines.
XX
XX      SO
XX      Sequence      6 AA;

Query Match      100.0%; Score 35; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.Be+05;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0.

OY      1 ELDKWA 6
        |||||

```

Db 1 ELDKMA 6

RESULT 4
AAW25868

ID AAW25868 standard; peptide; 6 AA.

AC AAW25868;

DT 20-OCT-1997 (first entry)

DE HIV-1 gp41 Kalinge's neutralisation epitope.

KM HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env;
V3 loop; vaccine; determinant; chimeric.

OS Synthetic.

PN US5639854-A.

PD 17-JUN-1997.

PF 09-JUN-1993; 93US-0073378.

PR 09-JUN-1994; 94US-0257528.

PR 09-JUN-1993; 93US-0073378.

(CONN-) CONNAUGHT LAB LTD.

PI Chong P, Klein MH, Sia CDY;

WPI; 1997-332082/30.

PT Tandem synthetic HIV peptide(s) useful as immunogens - comprising
gag protein T-cell epitope linked to env protein B-cell epitope

PS Example 1; Column 23-24; 41pp; English.

The invention relates to new synthetic peptides comprising at least one amino acid sequence comprising an HIV gag protein T-cell epitope linked at its C- or N-terminus to an amino acid sequence comprising a B-cell epitope of the V3 loop of an HIV env protein, which can be used to generate vaccines against HIV-1. The T-cell epitope sequence is pref. selected from the T-helper determinant core peptides P24E, P24N, P24L, P24M and P24H while the B-cell epitopes are derived from HIV strains including CTLB-56, V3MN, CTLB-29, CTLB-55, SP2, IAI, IIB, RF, Z6, 2054, 1714 and BX08. The peptides are chimeric and can be linked to a branched lys backbone. This is the sequence of the Kalinge's neutralisation epitope from the gp41 protein. The peptide is used in the construction of the chimeric T/B cell epitope peptides AAW25853-67.

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 18; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKMA 6

Db 1 ELDKMA 6

RESULT 5
AAW67384

ID AAW67384 standard; peptide; 6 AA.

AC AAW67384;

DT 25-JAN-1999 (first entry)

DE Kalinge's neutralisation epitope.

KM Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;

V3 loop.

Synthetic.
Human immunodeficiency virus type 1.

PN US5817754-A.

PD 06-OCT-1998.

PF 05-JUN-1995; 95US-0464329.

PR 09-JUN-1994; 94US-0257528.

PR 09-JUN-1993; 93US-0073378.

PR 05-JUN-1995; 95US-0464329.

(CONN-) CONNAUGHT LAB LTD.

PI Chong P, Klein MH, Sia CDY;

WPI; 1998-556461/47.

Synthetic human immunodeficiency virus-1 peptide(s) - containing
T-cell epitope and B-cell epitope(s) are candidate vaccines against
HIV-1

Disclosure; Column 21-22; 40pp; English.

The invention relates to a novel immunogenic composition for use in
vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
are generally designed based on the p24 core protein and the B-cell
epitopes from the V3 loop of the gp120 protein from various HIV-1
strains. This peptide represents the sequence of the Kalinge's
neutralisation epitope and is used to construct the hybrid peptides
AAW67381-W67383.

SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 19; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKMA 6

Db 1 ELDKMA 6

RESULT 6
AAW53143

ID AAW53143 standard; peptide; 6 AA.

AC AAW53143;

DT 20-JUL-1998 (first entry)

DE HIV gp41-contained antibody neutralisation epitope.

VJuno; HIV vaccine; codon usage optimisation; HIV; immune response;
human immunodeficiency virus; hepatitis; tuberculosis; tumour;
env protein; gp140 gene; recombinant.

Human immunodeficiency virus.

WO9748370-A2.

PD 24-DEC-1997.

PF 17-JUN-1997; 97WO-US10517.

PR 16-JUL-1996; 96GB-0014943.

PR 21-JUN-1996; 96US-0020165.

PR 16-JUL-1996; 96GB-0014942.

XX (MERI) MERCK & CO INC.
XX
XX Davies ME, Freed DC, Liu MA, Perry HC, Shiver JW;
XX WPI; 1998-062825/06.
XX
XX DNA encoding protein with codon usage optimised for intended host
PT cell - specifically for DNA vaccines against human immune deficiency
PT virus, allows rev-independent expression of HIV genes
XX
XX Example 7; Page 39; 113pp; English.
XX
XX This is the gp41-contained antibody neutralisation epitope retained in a
CC HIV gp140 vaccine construct. This is used in a Vlnneo expression vector
CC for vaccine production containing a new synthetic DNA, encoding a protein
CC or peptide. The synthetic DNA sequence encodes HIV env protein or its
CC fragment and has codons optimised for expression in a non-homologous
CC host. The synthetic DNA sequences are used to increase production of
CC recombinant protein and to induce anti-HIV neutralising antibody,
CC HIV-specific T-cell immune responses or protective immune responses in
CC vertebrates, specifically as HIV vaccines. Optimisation of codons
CC results in increased expression of the DNA in the host. The DNA induces
CC antigen-presenting cells to stimulate cytotoxic and helper T-cells, and
CC effector functions such as lymphokine secretion specific to HIV antigens.
CC Cross-strain protection is achieved without use of adjuvant and the
CC synthetic DNA may provide a longer-lasting response. The env gene
CC includes a high proportion of codons rarely used in mammals, so
CC optimisation will allow this gene to be expressed efficiently in absence
CC of rev. The DNA sequences, more generally, may express antigens from many
CC other pathogens, e.g. hepatitis or tuberculosis, and also from tumours.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 19; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 7
AA939717
ID AAY39717 standard; peptide; 6 AA.
XX
XX AAY39717;
XX
XX 26-NOV-1999 (first entry)
XX
XX HIV1 chimeric peptide gp41 epitope.
DE
XX HIV1 vaccine; immunogenic composition; T cell epitope; B cell epitope;
KW infection; antibody; antiviral.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX US5951986-A.
PN
XX 14-SEP-1999.
PD
XX 06-JUN-1995; 95US-0467881.
PF
XX 09-JUN-1994; 94US-0257528.
PR 09-JUN-1993; 93US-0073378.
XX
XX (CONN-) CONNAUGHT LAB LTD.
PA
XX Klein MH, Chong P, Sia CDY;
PI
XX WPI; 1999-550482/46.
DR
XX

PT Immunogenic composition containing synthetic fusion polypeptides
PT containing both the T and B cell epitopes of the human immunodeficiency
PT virus, useful antigens in producing vaccines
XX
XX Disclosure; Column 9; 43pp; English.
XX
XX This sequence represents a fragment of a HIV1 protein, and can be used in
CC the immunogenic composition of the invention. The composition comprises a
CC synthetic fusion polypeptide which includes a sequence encoding 1 or more
CC T cell epitopes and a sequence encoding 1 or more B cell epitopes and a
CC carrier. Both the T cell and B cell epitopes are derived from HIV
CC proteins. The compositions are useful as vaccines against HIV infection.
CC The composition induces HIV-1-specific polyclonal antibodies that are
CC opsonising and antiviral. The peptide components may be selected to
CC induce a response against different viral isolates and in subjects who
CC recognise different T cell epitopes.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 8
AAW99905
ID AAW99905 standard; peptide; 6 AA.
XX
XX AAW99905;
XX
XX 05-MAY-1999 (first entry)
XX
XX HIV-1 vaccine synthetic peptide SEQ ID NO:69.
DE
XX HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
XX
XX Synthetic.
OS
XX Human immunodeficiency virus type 1.
XX
XX US5876731-A.
PN
XX 02-MAR-1999.
PD
XX 05-JUN-1995; 95US-0462507.
PF
XX 09-JUN-1994; 94US-0257528.
PR 09-JUN-1993; 93US-0073378.
XX 05-JUN-1995; 95US-0462507.
XX
XX (CONN-) CONNAUGHT LAB LTD.
PA
XX Chong P, Klein MH, Sia CDY;
PI
XX WPI; 1999-189590/16.
DR
XX Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
PT epitope linked to gp41 B-cell epitope
XX
XX Claim 5; Column 72; 41pp; English.
XX
XX The present invention describes a synthetic peptide comprising an amino
CC acid sequence containing a T-cell epitope of an HIV gag protein linked
CC at its C terminus to an amino acid sequence containing a B-cell epitope
CC of an HIV gp41 protein and containing the amino acid sequence:
CC X1KDWX2; where X1 = E, A, G or Q, and X2 = A or T, or an amino acid
CC sequence capable of eliciting an HIV-specific antiserum and recognizing
CC the sequence X1KDWX2. The synthetic peptide is useful in vaccines
CC against HIV infection and in diagnostic applications. AAW98892 to

CC AAM98906, and AAM98989 to AAM99989 represent synthetic peptides from the
CC present invention.

XX Sequence 6 AA:

Query Match 100.0%; Score 35; DB 20; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|
|
|
|
|
|
DB 1 ELDKWA 6

RESULT 9
AAB24104
ID AAB24104 standard; peptide; 6 AA.

AC AAB24104;

DT 29-JAN-2001 (first entry)

DE HIV-1 gp41 epitope recognised by human Mab 2F5 SRQ ID NO:1.

XX HIV-1; human immunodeficiency virus; human; epitope; gp41; Mab;
KM monoclonal antibody; antiviral; antiHIV; infection; inhibition;
KW replication.

OS Human immunodeficiency virus type 1.

PN W0200055377-A1.

PD 21-SEP-2000.

PF 15-MAR-2000; 2000WO-US06771.

PR 17-MAR-1999; 99US-0124907.

PR 14-MAR-2000; 2000US-0525874.

XX (NYBL-) NEW YORK BLOOD CENT INC.
PA (JIAN/) JIANG S.
PA (DEBN/) DEBNATH A K.

PI Jiang S, Debnath AK;

DR WPI; 2000-656011/63.

XX Screening assay for antiviral compounds targeted to HIV-1 gp41 core
PT structure involves utilizing conformation-specific monoclonal antibody,
PT which is reactive with fusion active gp41 of the virus

XX Example 1c; Page 29; 79pp; English.

XX The present invention describes a method for screening (M1) an antiviral
CC compound (AC) targeted to the HIV-1 gp41 core structure. The method
CC involves capturing polyclonal antibodies (PAB) directed against trimer
CC of heterodimer (A) which contains N- and C-peptide (NP/CP) onto a
CC solid-phase, to form a PAB-coated solid-phase that is added with mixture
CC of NP, CP, and AC, adding monoclonal antibody (Mab) directed against (A)
CC and measuring the binding of Mab. The antivirals identified by the
CC method are useful for inhibiting HIV-1 replication or infectivity in
CC cells, in patients and for treating the patients infected with HIV-1.
CC The method distinguishes the anti-HIV-1 agents targeting the gp41 core
CC domain from those having different targets. Since the residues located
CC at the interaction sites in both the N-terminal heptad repeat (NHR) and
CC C-terminal heptad repeat (CHR) regions of gp41 are highly conserved, the
CC antiviral agents targeted to the gp41 core are considered to have
CC broader specificity against infection by HIV strains than those targeted
CC to gp120. The present sequence represents an HIV-1 gp41 epitope used in
CC an example from the present invention, which is recognised by the
CC human Mab 2F5.

XX Sequence 6 AA:
SQ

Query Match 100.0%; Score 35; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|
|
|
|
|
|
DB 1 ELDKWA 6

RESULT 10
AAV57748
ID AAV57748 standard; Peptide; 6 AA.

AC AAV57748;

DT 15-MAR-2000 (first entry)

DE Peptide amino acid sequence SEQ ID NO:46.

XX Recombinant negative strand viral RNA template; virus particle;
KM RNA directed RNA polymerase complex; expression; chimeric virus;
KW vaccine; packaging.

OS Unidentified.

PN US6001634-A.

PD 14-DEC-1999.

PF 29-JUN-1998; 98US-0106377.

PR 22-MAY-1990; 90US-0527237.

PR 01-JUN-1994; 94US-0252508.

PR 04-AUG-1992; 92US-0925061.

PR 28-AUG-1989; 89US-0399728.

PR 21-NOV-1989; 89US-0440053.

PR 01-FEB-1994; 94US-0190698.

XX (PALE/) PALESE P.
PA (GARC/) GARCIA-SASTRE A.

PI Palese P, Garcia-Sastre A;

DR WPI; 2000-071660/06.

XX Chimeric virus containing influenza virus RNA segments, useful for
PT expressing heterologous gene products in appropriate host cell systems

XX Disclosure; Column 73; 67pp; English.

XX The present invention describes a chimeric virus comprising influenza
CC virus containing a heterologous RNA segment from another strain of
CC influenza virus or 8 genomic segments from different strains of
CC influenza virus, with each segment comprising the reverse complement of
CC an RNA coding sequence operatively linked to a binding site specific for
CC a recombinant negative strand RNA polymerase of a negative strand RNA virus. The
CC heterologous gene products in appropriate host cell systems and/or to
CC construct recombinant viruses that express, package and/or present the
CC heterologous gene product. The expression products and chimeric viruses
CC may be used in vaccine formulations. AAV57746 to AAV57748, and AA256234
CC to AA256290, represent sequences used in the exemplification of the
CC present invention.

XX Sequence 6 AA:

Query Match 100.0%; Score 35; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|
|
|
|
|
|


```

XX OS Human immunodeficiency virus.
XX FN WO200154701-A1.
XX PD 02-AUG-2001.
XX PE 26-JAN-2001; 2001WO-US02766.
XX PR 31-JAN-2000; 2000US-0179276.
XX PA (AVET ) AVENTIS PASTEUR SA.
XX PA (AAR0-) AARON DIAMOND AIDS RES CENT.
XX PL Ho D, Markowitz M, Klein M, El Habib R;
XX DR WPI; 2001-488741/53.
XX PT Permitting cessation of antiviral therapy on HIV-infected patients
XX PT undergoing antiviral therapy, useful for treating HIV-infected
XX PT patients, by administering nucleic acid based vaccines encoding
XX PT HIV-specific immunogens
XX PS
XX PS Claim 29; Page 41; 57pp: English.
XX CC The invention relates to a method for permitting the cessation of
XX CC antiviral therapy in HIV-infected patients undergoing antiviral
XX CC therapy who have a controlled level of viraemia. The method involves
XX CC administration of nucleic-acid based vaccines encoding HIV-specific
XX CC immunogens to the patient's cells, enabling the expression of the HIV-specific
XX CC immunogens in the patient's cells. The HIV-specific antigens are
XX CC presented on major histocompatibility complex (MHC) class I and II
XX CC molecules, stimulating an HIV-specific CD8+ and CD4+ response. The
XX CC method permits the cessation of antiviral therapy on HIV-infected
XX CC patients either without virus rebound, with a delayed rebound, or
XX CC with decreased post-rebound set point, in addition to achieving
XX CC immunological control of persistent infectious virus after
XX CC discontinuation of antiviral therapy. The method is useful for people
XX CC who have lost their CD4+ and/or CD8+ T cell responses to HIV antigens,
XX CC such as those who have lost their proliferative T cell responses to
XX CC gp120 or p24. The method is specifically useful for treating persons
XX CC infected with a lymphotropic or immune-destroying retroviral infection,
XX CC or for treating HIV-infected patients undergoing anti-retroviral
XX CC therapy and having a viral load of less than 10000, preferably 1000
XX CC viral copies/ml of plasma and a CD4+ cell count of above 300 cells/ml,
XX CC preferably 500 cells/ml. The present sequence represents an HIV
XX CC epitope which may be encoded by a genetic vaccine of the invention.
XX SQ Sequence 6 AA:
XX
XX Query Match 100.0%; Score 35; DB 22; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX QY 1 ELDKWA 6
XX |||||
XX Db 1 ELDKWA 6
XX
XX RESULT 14
XX AAB92333
XX ID AAB92333 standard; Peptide; 6 AA.
XX
XX AAB92333;
XX
XX 22-JUN-2001 (first entry)
XX
XX Virus related peptide SEQ ID NO:1509.
XX
XX Protection: endogenous therapeutic peptide; peptidase; conjugation;
XX bIod component; modification; succinimidyI; maleimido group; amino;
XX hydroxyl; Ubiol; hormone; growth factor; neurotansmitter.
XX

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OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO20069900-A2.
PD	
PR	23-NOV-2000.
PF	
XX	
XX	17-MAY-2000; 2000WO-US13576.
XX	
PR	17-MAY-1999; 99US-0134406.
PR	10-SEP-1999; 99US-0153406.
PR	15-OCT-1999; 99US-0159783.
XX	
PA	(CONU-) CONUTCHEM INC.
XX	
PI	Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
DR	WPI; 2001-112059/12.
XX	
PT	Modifying and attaching therapeutic peptides to albumin prevents
PT	peptidase degradation, useful for increasing length of in vivo activity
XX	
PS	Disclosure; Page 699; 733pp; English.
CC	
CC	The present invention describes a modified therapeutic peptide (I)
CC	comprising a therapeutically active amino acid region (II) and a
CC	reactive group (III) (e.g. succinimide) and maleimido groups) attached to
CC	a less therapeutically active amino acid region (IV), which covalently
CC	bonds with amino/hydroxyl/thiol groups on blood components to form a
CC	peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC	(I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC	factors and neurotransmitters, to protect them from peptidase activity
CC	in vivo for the treatment of various disorders. Endogenous therapeutic
CC	peptides are not suitable as drug candidates as they require frequent
CC	administration due to rapid degradation by peptidases in the body.
CC	Modifying and attaching therapeutic peptides to albumin prevents or
CC	reduces the action of peptidases to increase length of activity (half
CC	life) and specifically as bonding to large molecules decreases
CC	intracellular uptake and interference with physiological processes.
CC	AAB90829 to AAB94441 represent peptides which can be used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 6 AA:
	Query Match 100.0%; Score 35; DB 22; Length 6;
	Best Local Similarity 100.0%; Pred. No. 7.8e+05;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY	
	1 ELDKWA 6
DB	1 ELDKWA 6
RESULT 15	
ID	AAG65282
AA	AAG65282 standard; peptide; 6 AA.
XX	
AC	AAG65282;
XX	
DT	30-NOV-2001 (first entry)
DE	
XX	HIV-1 isolate BH10 gp41 protein fragment (residues 662-667).
KW	
XX	HIV-1; gp120; BH10; vaccine; immunization; gp41 protein.
OS	
XX	Human immunodeficiency virus type 1.
XX	
PN	US6268484-B1.
XX	
PD	31-JUL-2001.
XX	
PF	30-JUL-1998; 98US-0124900.

XX 07-JUN-1995; 95US-0478536.
PR 19-APR-1995; 95WO-EP01481.
XX
XX (POLY-) POLYMER SCI IMMUNOBIOLOGISCHE FORSCHUNG.
PA Kattinger H, Buchacher A, Ernst W, Ballaun C, Pirtscher M,
PI Trkola A, Predl R, Schmalz C, Klima A, Steindl F, Muster T;
XX WPI; 2001-556601/62.
DR
XX
XX New anti-idiotypic antibodies consisting of one or both amino acid
PT sequences corresponding to amino acid positions 79-84 or 326-400 of the
PT processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1
PT infections
XX
XX
PS Disclosure; Column 1: 27pp; English.
XX
XX The invention relates to a peptide fragment comprising of amino acid
CC sequences corresponding to sequences within the processed gp120 of HIV-1
CC isolate BH10 (GenBank accession M15654). The peptides are useful in the
CC detection, prevention and treatment of HIV-1 infections, and in AIDS
CC therapy. The antibodies are especially useful as vaccines for active and
CC passive immunization, or for the detection and/or determination of HIV-1
CC infected cells and/or HIV-1 viruses. The present sequence represents the
CC HIV-1 isolate BH10 gp41 peptide fragment.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 35; DB 22; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||
Db 1 ELDKWA 6

Search completed: May 7, 2003, 09:53:54
Job time : 6.47222 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 2.02778 Seconds
(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-6

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	357	2 S21994	envelope protein g
2	35	100.0	357	2 S21996	envelope protein g
3	35	100.0	357	2 S21998	envelope protein g
4	35	100.0	357	2 S21998	envelope protein g
5	35	100.0	443	2 C41621	env polypeptide P
6	35	100.0	445	2 A41621	env polypeptide M
7	35	100.0	464	2 S59898	kynureninase (EC 3
8	35	100.0	464	2 T48675	kynureninase (EC 3
9	35	100.0	465	2 G02652	kynureninase (EC 3
10	35	100.0	817	2 T16409	hypothetical prote
11	35	100.0	846	2 VCLJND	env polypeptide pr
12	35	100.0	847	2 T09448	envelope glycoprote
13	35	100.0	847	2 S13289	env protein - huma
14	35	100.0	851	2 S33985	env polypeptide -
15	35	100.0	852	1 VCLJBR	envelope glycoprote
16	35	100.0	852	2 T12016	envelope glycoprote
17	35	100.0	853	2 S54384	env polypeptide pr
18	35	100.0	854	2 S13288	env protein - huma
19	35	100.0	855	2 VCLJAJ	env polypeptide pr
20	35	100.0	855	1 VCLJZR	env polypeptide pr
21	35	100.0	856	1 VCLJH3	env polypeptide pr
22	35	100.0	856	1 VCLJVL	env polypeptide pr
23	35	100.0	856	1 VCLJW	env polypeptide pr
24	35	100.0	859	1 VCLJMN	env polypeptide pr
25	35	100.0	859	2 T01672	envelope glycoprote
26	35	100.0	861	1 VCLJLV	env polypeptide pr
27	35	100.0	861	1 VCLJSC	env polypeptide pr
28	35	100.0	926	1 RDSFNN	nitrate reductase
29	32	91.4	268	2 T02448	hypothetical prote

30	32	91.4	326	2 E71561	probable solute pr
31	32	91.4	332	2 D71274	probable prolipopr
32	32	91.4	448	2 C83347	probable dipeptida
33	32	91.4	501	2 S51160	nitrate reductase
34	32	91.4	617	2 S19254	nitrate reductase
35	32	91.4	868	1 VCLJH4	env polypeptide -
36	32	91.4	889	2 T02240	nitrate reductase
37	32	91.4	912	1 RDBHNS	nitrate reductase
38	32	91.4	915	1 RDBHNS	nitrate reductase
39	32	91.4	916	2 S07554	nitrate reductase
40	32	91.4	1707	2 S77910	hypothetical prote
41	31	88.6	78	2 E82798	hypothetical prote
42	31	88.6	112	2 C64746	yaftu protein - Esc
43	31	88.6	126	2 H70387	hypothetical prote
44	31	88.6	151	2 AB0550	conserved hypothet
45	31	88.6	152	2 AH0368	conserved hypothet

ALIGNMENTS

RESULT 1
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21994, S70421
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STE1>
A:Cross-references: EMBL:X61355; NID:G60179; PID:CAA43622.1; PID:G60180
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MOID:92144209; PMID:1736940
A:Accession: S70421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>
A:Cross-references: EMBL:X61355; NID:G60179
C:Superfamily: type E retrovirus env polypeptide
Query Match 100.0%; Score 35; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 163 ELDKWA 168
RESULT 2
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuier, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MOID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61356; NID:G60181; PID:CAA43624.1; PID:G1067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 163 ELDKWA 168

RESULT 3

env polyprotein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

C:Accession: S70424; S21992

R:Stueller, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction

A:Reference number: S70417; PMID:1736940

A:Accession: S70424

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61358; NID:g60177; PIDN:CAA43628.1; PID:g60178

A:Experimental source: patient 22

A:Note: submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 163 ELDKWA 168

RESULT 4

env polyprotein gp120/gp41 - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000

C:Accession: S21998; S70425

R:Stueller, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction

A:Reference number: S21990

A:Accession: S21998

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <ST2>

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

R:Stueller, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction

A:Reference number: S70417; PMID:1736940

A:Accession: S70425

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-222, 'X', 224-358 <ST2>

A:Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 164 ELDKWA 169

RESULT 5

env polyprotein P - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999

C:Accession: C41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity in the C41621 strain

A:Reference number: A41621; PMID:92107924; PMID:1763038

A:Accession: C41621

A:Molecule type: DNA

A:Residues: 1-443 <BUR>

A:Cross-references: GB:M77230; NID:g328631; PIDN:AA803792.1; PID:g555015

A:Note: This virus was isolated from the mother's sexual partner

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:424-443/Domain: transmembrane #status predicted <TMN>

F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site:

Query Match 100.0%; Score 35; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 402 ELDKWA 407

RESULT 6

env polyprotein M - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999

C:Accession: A41621

R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991

A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity in the A41621 strain

A:Reference number: A41621; PMID:92107924; PMID:1763038

A:Accession: A41621

A:Molecule type: DNA

A:Residues: 1-445 <BUR>

A:Cross-references: GB:M77228; NID:g328627; PIDN:AA803790.1; PID:g555013

A:Note: this virus was isolated from the mother

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-253/Product: coat protein gp120 (fragment) #status predicted <GP1>

F:254-445/Product: coat protein gp41 (fragment) #status predicted <GP2>

F:426-445/Domain: transmembrane #status predicted <TMN>

F:9,23,42,48,78,85,101,107,131,137,143,147,152,155,190,205,353,358,367,379/Binding site:

Query Match 100.0%; Score 35; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 404 ELDKWA 409

RESULT 7
S59898
kynureninase (EC 3.7.1.3) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S59898
R:Takeuchi, F.; Tsudouchi, R.; Yoshino, M.; Shibata, Y.
B:Biochim. Biophys. Acta 1252, 185-188, 1995
A:Title: Amino-acid sequence of rat liver kynureninase.
A:Reference number: S59898; MWID:96049498; PMID:7578221
A:Accession: S59898
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-464 <RAK>
C:Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 90 ELDKWA 95

RESULT 8
T48675
kynureninase (EC 3.7.1.3) [validated] - rat
N:Alternate names: L-kynurenine hydrolase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C:Accession: T48675
R:Roma, S.; Nakamura, M.; Tonne, S.; Okuno, E.; Kido, R.; Breton, J.; Avanzi, N.; Cozzi, F.
FEBS Lett. 408, 5-10, 1997
A:Title: Cloning and recombinant expression of rat and human kynureninase.
A:Reference number: Z24527; MWID:97324088; PMID:9180257
A:Accession: T48675
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-464 <ROM>
A:Cross-references: EMBL:U68168; NID:g1532215; PIDN:AAC53206.1; PID:g1532216
A:Experimental source: liver
C:Function: A:Description: EC 3.7.1.3 [validated, MWID:97324088]
A:Pathway: biosynthesis of NAD cofactors
C:Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 464;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 90 ELDKWA 95

RESULT 9
G02652
kynureninase (EC 3.7.1.3) - human
N:Alternate names: L-kynurenine hydrolase
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C:Accession: G02652
R:Malherbe, P.
submitted to the EMBL Data Library, May 1996
A:Reference number: H01539
A:Accession: G02652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-465 <RAL>
A:Cross-references: EMBL:U57721; NID:g1323714; PIDN:AAC50650.1; PID:g1323715
C:Keywords: hydrolase

Query Match 100.0%; Score 35; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 90 ELDKWA 95

RESULT 10
T16409
hypothetical protein F48E8.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16409
R:Kirsten, J.
submitted to the EMBL Data Library, March 1995
A:Description: The sequence of C. elegans cosmid F48E8.
A:Reference number: S59413
A:Accession: T16409
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-817 <KIR>
A:Cross-references: EMBL:U23514; NID:g746484; PID:g746490; PIDN:AAC46543.1; CESP:F48E
A:Experimental source: strain Bristol N2
C:Genetics: A:Gene: CESP:F48E8.6
A:Introns: 107/3; 510/3; 670/3; 733/3

Query Match 100.0%; Score 35; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 359 ELDKWA 364

RESULT 11
VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV-1 NDK: a highly cytopathic strain of the human immunodeficiency virus type 1.
A:Reference number: J00065; MWID:90034200; PMID:2806917
A:Accession: J00066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA4873.1; PID:g328162
A:Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics: A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-25/Domain: signal sequence #status predicted <SID>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,

Query Match 100.0%; Score 35; DB 1; Length 846;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||

Db 652 ELDKMA 657

RESULT 12

T09448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JREF)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

C:Accession: T09448

R:Parag, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996

A:Reference number: 216673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAN>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 847;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6

Db 653 ELDKMA 658

RESULT 13

S13289

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A. Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13289; MUID:91043044; PMID:2172833

A:Accession: S13289

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 847;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6

Db 653 ELDKMA 658

RESULT 14

S33985

env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlino, F. submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77628.1; PID:g60199

C:Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 35; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6

Db 657 ELDKMA 662

RESULT 15

VC1JBR

env polyprotein - human immunodeficiency virus type 1 (isolate BR)

N:Alternate names: coat polyprotein

M:Contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997

C:Accession: A31667

R:Anand, R.; Thayer, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar

Virology 168, 79-89, 1989

A:Title: Biological and molecular characterization of human immunodeficiency virus (H

A:Reference number: A94389; MUID:89085613; PMID:2789516

A:Molecule type: DNA

A:Residues: 1-852 <ANA>

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; polyprotein; transmembrane protein

F:1-516/Product: coat protein gp120 #status predicted <CP1>

F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 100.0%; Score 35; DB 1; Length 852;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6

Db 658 ELDKMA 663

Search completed: May 7, 2003, 09:58:40

Job time: 3.02778 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:44:51 ; Search time 1.05556 Seconds
(without alignments)
235.760 Million cell updates/sec

Title: US-09-877-606-6
Perfect score: 35
Sequence: 1 ELDKMA 6

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	464	1 KYNU_RAT	P70712 rat mus nory
2	35	100.0	465	1 KYNU_HUMAN	Q16719 homo sapien
3	35	100.0	817	1 YR86_CAEEL	Q09568 caenorhabd
4	35	100.0	846	1 ENY_HV12L	P18799 human immun
5	35	100.0	847	1 ENY_HV1S1	P19550 human immun
6	35	100.0	847	1 ENY_HV1S2	P05880 human immun
7	35	100.0	848	1 ENY_HV1J2	P20871 human immun
8	35	100.0	851	1 ENY_HV1B8	P04582 human immun
9	35	100.0	852	1 ENY_HV1B1	P12488 human immun
10	35	100.0	852	1 ENY_HV1S3	P19549 human immun
11	35	100.0	853	1 ENY_HV1S1	P04581 human immun
12	35	100.0	853	1 ENY_HV1M1	P19551 human immun
13	35	100.0	853	1 ENY_HV1M2	P12487 human immun
14	35	100.0	855	1 ENY_HV1A2	P03378 human immun
15	35	100.0	855	1 ENY_HV1OY	P20888 human immun
16	35	100.0	855	1 ENY_HV1Z6	P04580 human immun
17	35	100.0	856	1 ENY_HV1B1	P03375 human immun
18	35	100.0	856	1 ENY_HV1H2	P04578 human immun
19	35	100.0	856	1 ENY_HV1H3	P04624 human immun
20	35	100.0	856	1 ENY_HV1H1	O70626 human immun
21	35	100.0	856	1 ENY_HV1M1	P05877 human immun
22	35	100.0	856	1 ENY_HV1P1	P03376 human immun
23	35	100.0	856	1 ENY_HV1S1	P05878 human immun
24	35	100.0	856	1 ENY_HV1M1	P04583 human immun
25	35	100.0	859	1 ENY_HV1M1	P03377 human immun
26	35	100.0	861	1 ENY_HV1B1	P04579 human immun
27	35	100.0	865	1 ENY_HV1H1	P23512 splinacia ol
28	35	100.0	926	1 NIA_SPTOL	Q98529 chlamydia t
29	32	91.4	326	1 Y067_CHLTR	O98524 streptomyce
30	32	91.4	332	1 IGT_TREPA	O31074 zea mays (m
31	32	91.4	358	1 T2S1_STRAH	P17571 zea mays (m
32	32	91.4	621	1 N1A1_MAIZE	P05882 human immun
33	32	91.4	863	1 ENY_HV1Z8	

34	32	91.4	868	1 ENY_HV1C4	P05879 human immun
35	32	91.4	889	1 N1A3_MAIZE	P49102 zea mays (m
36	32	91.4	912	1 N1A2_HORVU	P27969 hordeum vul
37	32	91.4	915	1 N1A1_HORVU	P27967 hordeum vul
38	32	91.4	916	1 N1A1_ORYSA	P16081 oryza sativ
39	32	91.4	1073	1 ACA9_ARATH	Q91041 arabidopsis
40	31	88.6	112	1 YAFU_ECOLI	P77354 escherichia
41	31	88.6	381	1 DHB2_MOUSE	P51658 mus musculu
42	31	88.6	388	1 GAG_HV1W2	P05889 human immun
43	31	88.6	421	1 ECB2_HAHEL	O52250 halomonas e
44	31	88.6	498	1 GAG_HV1OY	P20889 human immun
45	31	88.6	499	1 GAG_HV1N5	P12493 human immun

ALIGNMENTS

RESULT 1
ID KYNU_RAT STANDARD; PRT; 464 AA.
AC P70712; O9GW90;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
GN KYNU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN (1)
RP SEQUENCE, AND MASS SPECTROMETRY.
RC STRAIN=WiStar; TISSUE=Liver;
RX MEDLINE=96049498; PubMed=7578221;
RA Takeuchi F., Teubouchi R., Yoshino M., Shibata Y.;
RT "Amino acid sequence of rat liver kynureninase.";
RL Biochim. Biophys. Acta 1252:185-188(1995).
RN (2)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=97324088; PubMed=9180257;
RA Toma S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,
AVANCI N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;
RT "Cloning and recombinant expression of rat and human kynureninase.";
RL FEBS Lett. 408:5-10(1997).
RN (3)
RP SEQUENCE OF 19-117 FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96314506; PubMed=8706755;
RA Alberati-Giani D., Buchli R., Malherbe P., Broger C., Lang G.,
Koehler C., Lahm H.-W., Cesura A.M.;
RT "Isolation and expression of a cDNA clone encoding human
kynureninase.";
RL Eur. J. Biochem. 239:460-468(1996).
RN (4)
RP FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE (L-KYN) AND L-3-
HYDROXYKYNURENINE (L-3OHKYN) INTO ANTHRANILIC (AA) AND 3-
HYDROXYANTHRANILIC ACIDS (3-OHAA), RESPECTIVELY. HAS A PREFERENCE
FOR THE L-3-HYDROXY FORM. OPTIMUM ACTIVITY IS AROUND PH 9.0 FOR L-
KYN AND AROUND 8.5 FOR L-3OHKYN. ALSO HAS CYSTEINE-CONJUGATE-
BETA-LASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = anthranilate + L-
alanine.
CC -1- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)O = 3-
hydroxyanthranilate + L-alanine.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- ENZYME REGULATION: INHIBITED BY O-METHYLBENZOTLANTANINE (OMBA).
CC -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS FROM
TRYPTOPHAN THROUGH THE KYNURENINE PATHWAY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN LIVER AND KIDNEY. ALSO
DETECTED IN HEART, RETINA, OVARY, LUNG, TESTIS AND BRAIN.
CC -1- INDUCTION: INHIBITED BY THIOL REAGENTS AND HEAVY METAL IONS.

CC -1- SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELATED
 CC TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
 CC -----
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 CC -----
 DR EMBL: U68168; AAC53206.1; -
 KM Hydroxylase; Pyridoxal phosphate; Acetylation.
 FT BINDING 1 1
 FT MOD_RES 1 1
 FT BINDING 276 276 PYRIDOXAL PHOSPHATE.
 FT CONFLICT 18 18 A -> T (IN REF. 1).
 FT CONFLICT 26 26 D -> N (IN REF. 1).
 FT CONFLICT 118 118 T -> S (IN REF. 1).
 SQ SEQUENCE 464 AA; 52453 MW; EFIC95E3202EC6C CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 464;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 Db 90 ELDKWA 95
 RESULT 2
 KYNH_HUMAN
 ID KYNH_HUMAN STANDARD; PRT; 465 AA.
 AC Q16719;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kynureninase (EC 3.7.1.3) (L-kynurenine hydrolase).
 GN KYNH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
 RC TISSUE-Hepatoma;
 RX MEDLINE=96314506; PubMed=8706755;
 RA Alberati-Fiani D., Buchli R., Malherbe P., Broger C., Lang G.,
 RT Koehler C., Lahm H.-W., Cesura A.M.;
 RT "Isolation and expression of a cDNA clone encoding human
 RT kynureninase.";
 RL Eur. J. Biochem. 239:460-468(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=97324088; PubMed=9180257;
 RA Toma S., Nakamura M., Tone S., Okuno E., Kido R., Breton J.,
 RT Avanzi N., Cozzi L., Speciale C., Mostardini M., Gatti S., Benatti L.;
 RL FEBS Lett. 408:5-10(1997).
 CC -1- FUNCTION: CATALYZES THE CLEAVAGE OF L-KYNURENINE (L-KYN) AND L-3-
 CC HYDROXYKYNURENINE (L-3OHKYN) INTO ANTHRANILIC (AA) AND 3-
 CC HYDROXYKYNURENINIC ACIDS (3-OHAA), RESPECTIVELY. HAS A PREFERENCE
 CC FOR THE L-3-HYDROXY FORM. ALSO HAS CYSTEINE-CONJUGATE-BETA-LYASE
 CC ACTIVITY (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: L-kynurenine + H(2)O = anthranilate + L-
 CC alanine.
 CC -1- CATALYTIC ACTIVITY: L-3-hydroxykynurenine + H(2)O = 3-
 CC hydroxyanthranilate + L-alanine.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- ENZYME REGULATION: INHIBITED BY O-METHOXYBENZYLALANINE (OMBA).
 CC -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF NAD COFACTORS FROM
 CC TRYPTOPHAN THROUGH THE KYNURENINE PATHWAY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES TESTED (HEART, BRAIN
 CC PLACENTA, LUNG, LIVER, SKELETAL MUSCLE, KIDNEY AND PANCREAS).
 CC HIGHEST LEVELS FOUND IN PLACENTA, LIVER AND LUNG. EXPRESSED IN
 CC ALL BRAIN REGIONS.
 CC -1- INDUCTION: INCREASED LEVELS IN SEVERAL CEREBRAL AND SYSTEMIC
 CC INFLAMMATORY CONDITIONS.
 CC -1- SIMILARITY: BELONGS TO THE KYNURENINASE FAMILY. SLIGHTLY RELATED
 CC TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
 CC -----
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 CC -----
 DR EMBL: U57721; AAC50650.1; -
 DR Genew; HGNC:6469; KYNH.
 DR MIM: 605197; -
 DR MIM: 236800; -
 KM Hydroxylase; Pyridoxal phosphate; Acetylation.
 FT MOD_RES 1 1
 FT BINDING 276 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 465 AA; 52351 MW; BDD136BE18C79EBB CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 465;
 Best Local Similarity 100.0%; Pred. No. 8.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELDKWA 6
 Db 90 ELDKWA 95
 RESULT 3
 YR86_CAEEL
 ID YR86_CAEEL STANDARD; PRT; 817 AA.
 AC Q09568;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein F48E8.6 in chromosome III.
 DE Hypothetical protein F48E8.6.
 GN F48E8.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Kirsten J.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U23514; AAC46543.1; -
 DR Mornep; F48E8.6; CE02758.
 DR InterPro: IPR001900; Ribonuclease_II.
 DR Pfam: PF00773; RNB; 1.
 DR PROSITE: PS01175; RIBONUCLEASE_II; 1.
 KM Hypothetical protein; Hydrolase; Nuclease.
 SQ SEQUENCE 817 AA; 93727 MW; 9BE5B06162699243 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 817;

FT CAROHD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA: 96135 MW: 0A901317FD7FE2AB CRC64;

Query Match 100.0%; Score 35; DB 1; Length 847;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
 DB 653 ELDKWA 658

ENV_HV1W2 STANDARD; PRT: 847 AA.
 AC P05880;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11705;
 RN [1]

RP SEQUENCE FROM N.A. MEDLINE=86235450; PubMed=3012778;
 RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
 RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
 RT "Genetic variation in HTLV-III/LAV over time in patients with AIDS or at risk for AIDS."
 RL Science 232:1548-1553(1986).
 CC -i- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.

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CC EMBL; M12507; AAB12990.1; -
 DR HIV; M12507; ENV5WMJ2.
 DR InterPro; IPR000328; ENV_GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Transmembrane;
 FT SIGNAL.
 FT CHAIN 1 29
 FT CHAIN 30 501
 FT CHAIN 502 847
 FT DISULFID 53 73
 FT DISULFID 118 202
 FT DISULFID 125 193
 FT DISULFID 130 152
 FT DISULFID 215 244
 FT DISULFID 225 236
 FT DISULFID 235 326
 FT DISULFID 372 435
 FT DISULFID 379 408
 FT CAROHD 87 87
 FT CAROHD 134 134
 FT CAROHD 140 140
 FT CAROHD 151 151
 FT CAROHD 155 155
 FT CAROHD 183 183
 FT CAROHD 184 184
 FT CAROHD 194 194
 FT CAROHD 231 231
 FT CAROHD 238 238
 FT CAROHD 259 259
 FT CAROHD 273 273
 FT CAROHD 286 286
 FT CAROHD 292 292
 FT CAROHD 327 327
 FT CAROHD 334 334
 FT CAROHD 350 350
 FT CAROHD 356 356
 FT CAROHD 380 380
 FT CAROHD 386 386
 FT CAROHD 390 390
 FT CAROHD 400 400
 FT CAROHD 438 438
 FT CAROHD 450 450
 FT CAROHD 602 602
 FT CAROHD 607 607
 FT CAROHD 616 616
 FT CAROHD 628 628
 SQ SEQUENCE 847 AA: 96466 MW: CD1E33D73AABCBAC CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 847;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
 DB 653 ELDKWA 658

ENV_HV1JR STANDARD; PRT: 848 AA.
 AC P20871;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11688;
 RN [1]

RP SEQUENCE FROM N.A. KOYANAGI S., CHEN I.S.Y.;
 RA Submitted (DEC-1988) to the HIV data bank.

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EMBL: M38429; AAB03749.1; -
 DR HIV; M38429; ENV5JRCSE.
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00517; GP41; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL. 1 32
 FT CHAIN 504 503
 FT CHAIN 504 503
 FT DISULFID 53 73
 FT DISULFID 118 203
 FT DISULFID 125 194
 FT DISULFID 130 154
 FT DISULFID 216 245
 FT DISULFID 226 237
 FT DISULFID 284 328
 FT DISULFID 374 437
 FT DISULFID 381 410
 FT CARBOHYD 87 87
 FT CARBOHYD 134 134
 FT CARBOHYD 137 137
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 185 185
 FT CARBOHYD 195 195
 FT CARBOHYD 228 228
 FT CARBOHYD 239 239
 FT CARBOHYD 260 260
 FT CARBOHYD 274 274
 FT CARBOHYD 287 287
 FT CARBOHYD 293 293
 FT CARBOHYD 299 299
 FT CARBOHYD 329 329
 FT CARBOHYD 336 336
 FT CARBOHYD 352 352
 FT CARBOHYD 382 382
 FT CARBOHYD 388 388
 FT CARBOHYD 392 392
 FT CARBOHYD 403 403
 FT CARBOHYD 440 440
 FT CARBOHYD 453 453
 FT CARBOHYD 603 603
 FT CARBOHYD 608 608
 FT CARBOHYD 617 617
 FT CARBOHYD 629 629
 FT CARBOHYD 808 808
 FT CARBOHYD 808 808
 FT SEQUENCE 848 AA; 96475 MW; 2076751227EC3F3 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 848;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentiviridae.
 NCBI_TaxID:11684;
 RN
 RP
 RX MEDLINE:85111123; PubMed:2578615;
 RA Ratner L., Haseltine W., Patarca R., Lyaak K.J., Starcich B.R., Josephs S.F., Doran E.R., Ratsalki J.A., Whitehorn E.A., Baumanster K., Ivanoff U., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Papas T.S., Ghayee J., Chang N.T., Gallo R.C., Wong-Staal F.;
 RA "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RA Nature 313:277-284(1985).
 CC
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EMBL: K02011; AAA44661.1; -
 DR HIV; K02011; ENV5B8.
 DR GLYCOSULEDB: P04582; -
 DR InterPro: IPR000328; Env-GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR AIDS; Coat protein; Glycoprotein; Transmembrane;
 KM Signal.
 FT SIGNAL. 1 30
 FT CHAIN 507 506
 FT CHAIN 507 506
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 440
 FT DISULFID 385 413
 FT CARBOHYD 88 88
 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
 FT CARBOHYD 160 160
 FT CARBOHYD 186 186
 FT CARBOHYD 197 197
 FT CARBOHYD 220 230
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 332 332
 FT CARBOHYD 339 339
 FT CARBOHYD 356 356
 FT CARBOHYD 386 386
 FT CARBOHYD 392 392
 FT CARBOHYD 401 401
 FT CARBOHYD 443 443
 FT CARBOHYD 458 458
 FT CARBOHYD 606 606
 FT CARBOHYD 611 611
 FT CARBOHYD 620 620
 FT CARBOHYD 632 632
 FT CARBOHYD 669 669
 FT SEQUENCE 507 AA; 506 MW; 2076751227EC3F3 CRC64;
 Query Match 100.0%; Score 35; DB 1; Length 507;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FT	CARBOHYD	745	745	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	811	811	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	851 AA:	96644 MW;	D16A390857785F1 CRC64;
	Query Match	100.0%;	Score 35;	DB 1; Length 851;
	Best Local Similarity	100.0%;	Pred. No. 16;	
	Matches 6;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	1 ELDKWA 6			
Db	657 ELDKWA 662			
	RESULT 9			
ENV_HV1BN				
ID	ENV_HV1BN	STANDARD:	PRT:	852 AA.
AC	P12488:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCHL_TaxID=11693;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89085613; PubMed=2789516;			
RA	Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.;			
RT	"Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia.";			
RT	Virology 168:79-89(1989).			
RL	-I- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.			
CC	-----			
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CC	-----			
DR	EMBL; M21098; AAA44221.1; -.			
DR	PIR; A31667; VCLJBR.			
DR	HIV; M21098; ENVSBRVA.			
DR	InterPro; IPR000328; Env GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL.	1	30	
FT	CHAIN	31	507	
FT	CHAIN	508	852	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	155	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	330	BY SIMILARITY.
FT	DISULFID	376	439	BY SIMILARITY.
FT	DISULFID	383	412	BY SIMILARITY.
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match	Best Local Similarity	100.0%	Score 35;	DB 1;	Length 852;
Matches 6;	Conservative	0;	Mismatches	0;	Gaps 0;
Oy	1 ELDKWA 6				
Db	658 ELDKWA 663				
RESULT 10					
ID	ENV_HV1S3	STANDARD:	PRT:	852 AA.	
AC	P19549;				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-FEB-1991 (Rel. 17, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].				
GN	ENV.				
OS	Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirae.				
OX	NCBI_TaxID=11690;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=90317906; PubMed=2370688;				
RA	York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;				
RT	"Human immunodeficiency virus type 1 cellular host range,				
RT	replication, and cytopathicity are linked to the envelope region of				
RT	the viral genome."				
RL	J. Virol. 64:4016-4020(1990).				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M38427; AAA45067.1; -.				
DR	HIV; M38427; ENV5SE33.				
DR	InterPro; IPR000328; ENV_GP41.				
DR	InterPro; IPR000777; GP120.				
DR	Pfam; PF00516; GP120; 1.				
DR	Pfam; PF00517; GP41; 1.				
KW	AIDS; Coat protein; Polypeptide; Polypeptide; Glycoprotein; Transmembrane;				
FT	Signal.				
FT	SIGNAL				

FT CHAIN 32 506 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 507 852 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 156 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 331 BY SIMILARITY.
 FT DISULFID 377 439 BY SIMILARITY.
 FT DISULFID 384 412 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;

Query Match 100.0%; Score 35; DB 1; Length 852;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
 DB 658 ELDKWA 663

RESULT 11
 ENV_HYIEM STANDARD; PRT; 853 AA.
 AC P04581.1
 DT 13-AUG-1987 (rel. 05, Created)
 DT 13-AUG-1987 (rel. 05, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)]
 GN ENV.
 OS Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID-11689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86245056; PubMed=2424612;
 RA Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
 RT "Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients."
 RL Cell 46:63-74(1986).
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 CC or send an email to license@sib.ch).
 CC -----
 DR EMBL: K03454; AAA44329.1; -
 DR EMBL: A07108; CAA00616.1; -
 DR HIV: K03454; ENVSELI.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 CC Aids; Coat protein; Glycoprotein; Transmembrane;
 KW Signal.
 FT CHAIN 1 31 BY SIMILARITY.
 FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 206 BY SIMILARITY.
 FT DISULFID 125 197 BY SIMILARITY.
 FT DISULFID 130 154 BY SIMILARITY.
 FT DISULFID 219 248 BY SIMILARITY.
 FT DISULFID 229 240 BY SIMILARITY.
 FT DISULFID 297 330 BY SIMILARITY.
 FT DISULFID 376 442 BY SIMILARITY.
 FT DISULFID 383 416 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA; 96721 MW; F9CD864DDA0D07A5 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 853;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
 DB 659 ELDKWA 664

RESULT 12
 ENV_HYIEM STANDARD; PRT; 853 AA.
 ID ENV_HYIEM

FT	CARBOHYD	635	635	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
FT	CARBOHYD	672	672	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
FT	CARBOHYD	748	748	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
FT	CARBOHYD	814	814	N-LINKED (GLCNAC. . .)	(POTENTIAL).				
SO	SEQUENCE	853 AA:	96912 MW:	3377B93B6F22ABA	CRC64:				
Query Match		100.0%;	Score 35;	DB 1;	Length 853;				
Best Local Similarity		100.0%;	Pred. No. 16;						
Matches 6;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;				
OY	1 ELDKMA 6								
DB	660 ELDKMA 665								
RESULT 13									
ENV_HV122									
ID	ENV_HV122	STANDARD:	PRT:	853 AA.					
AC	P12487;								
DT	01-OCT-1989 (Rel. 12, Created)								
DT	01-OCT-1989 (Rel. 12, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	Envelope polypeptide GP160 precursor [Contents: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP11)].								
DE	glycoprotein (GP120); Transmembrane glycoprotein (GP11)].								
GN	ENV.								
OS	Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).								
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.								
OX	NCBI_Taxid-11683;								
RM	[1]								
RP	SEQUENCE FROM N.A.								
RA	Theodore T., Buckler-White A.;								
RL	Submitted (NOV-1988) to the HIV data bank.								
CC	-----								
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/1sb-sib.ch/).								
CC	or send an email to license@1sb-sib.ch).								
CC	-----								
DR	EMBL; M22639; AAA45370.1; -.								
DR	HIV; M22639; ENV52286.								
DR	InterPro; IPR000328; Env_GP41.								
DR	InterPro; IPR000777; GP120.								
DR	Pfam; PF00516; GP120; 1.								
KW	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;								
KW	Signal.								
FT	SIGNAL.	1	31						
FT	CHAIN	32	508						
FT	CHAIN	509	853						
FT	DISULFID	53	73						
FT	DISULFID	118	206						
FT	DISULFID	125	197						
FT	DISULFID	130	154						
FT	DISULFID	219	248						
FT	DISULFID	229	240						
FT	DISULFID	297	330						
FT	DISULFID	376	442						
FT	DISULFID	383	415						
FT	CARBOHYD	87	87						
FT	CARBOHYD	137	137						
FT	CARBOHYD	144	144						
FT	CARBOHYD	153	153						
FT	CARBOHYD	157	157						
FT	CARBOHYD	185	185	</					

FT CARBOHD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 441 441 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 853 AA; 97043 MW; 849B08CBAFF7008 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 853;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
DB 659 ELDKWA 664

ENV_HV1A2 STANDARD; PRT; 855 AA.
ID ENV_HV1A2 STANDARD; PRT; 855 AA.

AC P03378;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2)."
RL Science 227:484-492(1985).

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DR EMBL; K02007; AAB59882.1; .
DR PIR; A03976; VCLA2.
DR HIR; K02007; ENV5SF2.
DR InterPro: IPR000328; ENV_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam; PF00515; GP120.1.
DR Pfam; PF00517; GP41.1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
KW Signal.
KW SIGNAL.
FT CHAIN 1 29
FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 208 BY SIMILARITY.
FT DISULFID 125 199 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 221 250 BY SIMILARITY.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 299 333 BY SIMILARITY.
FT DISULFID 380 442 BY SIMILARITY.
FT DISULFID 387 415 BY SIMILARITY.
FT CARBOHD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 298 298 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 358 358 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 364 364 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
DB 661 ELDKWA 666

ENV_HV10Y STANDARD; PRT; 855 AA.
ID ENV_HV10Y STANDARD; PRT; 855 AA.

AC P20888;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.

OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=90148544; PubMed=2559749;
RA Hueb T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).

CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC -----

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CC or send an email to license@sib-sib.ch).

DR EMBL; M26727; AA83397.1; -.
DR HIV; M26727; ENVSOYL.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120.1.
DR Pfam; PF00517; GP41.1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 210 BY SIMILARITY.
FT DISULFID 125 201 BY SIMILARITY.
FT DISULFID 130 162 BY SIMILARITY.
FT DISULFID 223 252 BY SIMILARITY.
FT DISULFID 233 244 BY SIMILARITY.
FT DISULFID 301 335 BY SIMILARITY.
FT DISULFID 381 442 BY SIMILARITY.
FT DISULFID 388 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 281 281 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 399 399 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 815 815 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607ADD62DA CRC64;

Query Match 100.0%; Score 35; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
Db 661 ELDKWA 666

Search completed: May 7, 2003, 09:54:38
Job time : 2.05556 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 4.30556 Seconds
(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-6

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	34	15	069893 human immun
2	35	100.0	34	15	069894 human immun
3	35	100.0	34	15	069903 human immun
4	35	100.0	34	15	069904 human immun
5	35	100.0	34	15	069905 human immun
6	35	100.0	41	15	069891 human immun
7	35	100.0	41	15	069892 human immun
8	35	100.0	42	15	069910 human immun
9	35	100.0	49	15	069895 human immun
10	35	100.0	49	15	069896 human immun
11	35	100.0	49	15	069906 human immun
12	35	100.0	49	15	069907 human immun
13	35	100.0	49	15	069909 human immun
14	35	100.0	50	15	069898 human immun
15	35	100.0	57	15	069911 human immun
16	35	100.0	57	15	069912 human immun

17	35	100.0	57	15	069913 human immun
18	35	100.0	117	15	09YXW7 human immun
19	35	100.0	117	15	09YXW1 human immun
20	35	100.0	117	15	09YRS9 human immun
21	35	100.0	117	15	09YRS2 human immun
22	35	100.0	117	15	09QON5 human immun
23	35	100.0	118	15	09Y202 human immun
24	35	100.0	118	15	09E553 human immun
25	35	100.0	118	15	09E552 human immun
26	35	100.0	118	15	09E5R1 human immun
27	35	100.0	122	15	09YXR8 human immun
28	35	100.0	122	15	09YXR7 human immun
29	35	100.0	122	15	09YXR6 human immun
30	35	100.0	122	15	09YXR4 human immun
31	35	100.0	122	15	09YXR2 human immun
32	35	100.0	122	15	09YXR1 human immun
33	35	100.0	122	15	09YXR0 human immun
34	35	100.0	122	15	09YXR8 human immun
35	35	100.0	122	15	09YXR6 human immun
36	35	100.0	122	15	09YXQ2 human immun
37	35	100.0	122	15	09YXQ1 human immun
38	35	100.0	122	15	09YXQ0 human immun
39	35	100.0	122	15	09YXP7 human immun
40	35	100.0	122	15	09YXP4 human immun
41	35	100.0	122	15	09YXP2 human immun
42	35	100.0	122	15	09YXP1 human immun
43	35	100.0	122	15	09YXP0 human immun
44	35	100.0	122	15	09YXN9 human immun
45	35	100.0	122	15	09YXN5 human immun
					09YXN4 human immun

ALIGNMENTS

RESULT 1
ID 069893 PRELIMINARY; PRT: 34 AA.
AC 069893;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94211861; PubMed-7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emml E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; 006723; AAA19136.1;
DR InterPro; IPR000328; Env_Gp41.
DR Pfam; PF00517; Gp41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
Db 23 ELDKWA 28

RESULT 2

069894 ID 069894 PRELIMINARY; PRT; 34 AA.
AC 069894;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06724; AAA19137.1; -;
DR InterPro; IPR000328; Env_GP41.
KW Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 23 ELDKWA 28

RESULT 3
069903 ID 069903 PRELIMINARY; PRT; 34 AA.
AC 069903;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06733; AAA19146.1; -;
DR InterPro; IPR000328; Env_GP41.
KW Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 23 ELDKWA 28

RESULT 4
069904 ID 069904 PRELIMINARY; PRT; 34 AA.
AC 069904;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06734; AAA19147.1; -;
DR InterPro; IPR000328; Env_GP41.
KW Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4184 MW; B81CAA65F131AD5A CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 23 ELDKWA 28

RESULT 5
069905 ID 069905 PRELIMINARY; PRT; 34 AA.
AC 069905;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06735; AAA19148.1; -;
DR InterPro; IPR000328; Env_GP41.
KW Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 100.0%; Score 35; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 23 ELDKWA 28

OY 1 ELDKMA 6
|||||
DB 23 ELDKMA 28

RESULT 6

O69891 PRELIMINARY; PRT; 41 AA.
AC O69891;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP41 (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL: U06721; AAA19134.1; -;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 41
SQ SEQUENCE 41 AA; 5082 MW; 0B9C7E2CDD403CC6 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6
|||||
DB 23 ELDKMA 28

RESULT 7
O69892 PRELIMINARY; PRT; 41 AA.
AC O69892;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP41 (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL: U06722; AAA19135.1; -;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 41
SQ SEQUENCE 41 AA; 5081 MW; 0B9C70CC3403CC6 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 41;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6
|||||
DB 23 ELDKMA 28

RESULT 8

O69910 PRELIMINARY; PRT; 42 AA.
AC O69910;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP41 (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL: U06740; AAA19153.1; -;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 5248 MW; 613E1B2DBB31A722 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 42;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKMA 6
|||||
DB 31 ELDKMA 36

RESULT 9
O69895 PRELIMINARY; PRT; 49 AA.
AC O69895;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
GN GP41 (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL: U06725; AAA19138.1; -;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 49

SO SEQUENCE 49 AA; 6168 MW; 8077C4815B8D26FE CRC64;
Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ELDKWA 6
|||||
DB 38 ELDKWA 43
RESULT 10
Q69896 PRELIMINARY; PRT; 49 AA.
AC Q69896;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; 006726; AAA19139.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;
Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ELDKWA 6
|||||
DB 38 ELDKWA 43
RESULT 11
Q69906 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; 006736; AAA19149.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.

KW Transmembrane.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8BC7CDD8 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ELDKWA 6
|||||
DB 38 ELDKWA 43
RESULT 12
Q69907 PRELIMINARY; PRT; 49 AA.
AC Q69907;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; 006737; AAA19150.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6241 MW; 29C4E5A8BC7CDD8 CRC64;
Query Match 100.0%; Score 35; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ELDKWA 6
|||||
DB 38 ELDKWA 43
RESULT 13
Q69909 PRELIMINARY; PRT; 49 AA.
AC Q69909;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Gp41 (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
variants and primary isolates by IAM-41-2F5, an anti-gp41 human
monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

DR EMBL: U06739; AAA19152.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 49 49
 SO SEQUENCE 49 AA; 6196 MW; E9B61825B832D1E CRC64;

Query Match 100.0%; Score 35; DB 15; Length 49;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
 DB 38 ELDKWA 43

RESULT 14

ID 069898 PRELIMINARY; PRT; 50 AA.

AC 069898; 01-NOV-1996 (TREMUREL. 01, Created)

DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)

DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)

DE Gp41 (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94211861; PubMed-7512731;

RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

*Neutralization of divergent human immunodeficiency virus type 1

RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human

monoclonal antibody.*

RT Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

RL EMBL: U06728; AAA19141.1; -;

DR InterPro: IPR000328; Env_Gp41.

DR Pfam: PF00517; Gp41; 1.

KW Transmembrane.

FT NON_TER 1 1

FT NON_TER 50 50

SO SEQUENCE 50 AA; 6358 MW; EABA093A1C6C79E1 CRC64;

Query Match 100.0%; Score 35; DB 15; Length 50;

Best Local Similarity 100.0%; Pred. No. 6.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6

DB 39 ELDKWA 44

RESULT 15

ID 069911

AC 069911; PRELIMINARY; PRT; 57 AA.

DT 01-NOV-1996 (TREMUREL. 01, Created)

DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)

DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)

DE Gp41 (Fragment).

GN ENV.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94211861; PubMed-7512731;

RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,

Keller P.M., Shaw A.R., Emini E.A.;

*Neutralization of divergent human immunodeficiency virus type 1

RT variants and primary isolates by IAM-41-2P5, an anti-gp41 human

monoclonal antibody.*

RT Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).

DR EMBL: U06741; AAA19154.1; -;

DR InterPro: IPR000328; Env_Gp41.

DR Pfam: PF00517; Gp41; 1.

KW Transmembrane.

FT NON_TER 1 1

FT NON_TER 57 57

SO SEQUENCE 57 AA; 7267 MW; C2BC6A9034525CAE CRC64;

Query Match 100.0%; Score 35; DB 15; Length 57;
 Best Local Similarity 100.0%; Pred. No. 7.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
 DB 46 ELDKWA 51

Search completed: May 7, 2003, 09:57:20
 Job time: 4.30556 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 1.77778 Seconds
(without alignments)
99.302 Million cell updates/sec

Title: US-09-877-606-6

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	100.0	6	1	US-08-257-528B-69	Sequence 69, Appl
2	35	100.0	6	1	US-08-361-479-1	Sequence 1, Appl
3	35	100.0	6	1	US-08-473-576-1	Sequence 1, Appl
4	35	100.0	6	1	US-08-460-602A-69	Sequence 69, Appl
5	35	100.0	6	1	US-08-323-192D-47	Sequence 47, Appl
6	35	100.0	6	1	US-08-463-966A-69	Sequence 69, Appl
7	35	100.0	6	1	US-08-465-217A-69	Sequence 69, Appl
8	35	100.0	6	2	US-08-464-329A-69	Sequence 69, Appl
9	35	100.0	6	2	US-08-021-879-1	Sequence 69, Appl
10	35	100.0	6	2	US-08-470-887A-46	Sequence 46, Appl
11	35	100.0	6	2	US-08-252-508B-46	Sequence 46, Appl
12	35	100.0	6	2	US-08-975-699-23	Sequence 23, Appl
13	35	100.0	6	2	US-08-417-210A-147	Sequence 147, App
14	35	100.0	6	2	US-08-843-718-1	Sequence 1, Appl
15	35	100.0	6	2	US-08-462-507A-69	Sequence 69, Appl
16	35	100.0	6	2	US-08-972-089-23	Sequence 23, Appl
17	35	100.0	6	2	US-08-467-881A-69	Sequence 69, Appl
18	35	100.0	6	4	US-09-106-377-46	Sequence 46, Appl
19	35	100.0	6	4	US-09-124-900-11	Sequence 11, Appl
20	35	100.0	7	1	US-08-257-528B-98	Sequence 98, Appl
21	35	100.0	7	1	US-08-460-602A-98	Sequence 98, Appl
22	35	100.0	7	1	US-08-463-966A-98	Sequence 98, Appl
23	35	100.0	7	1	US-08-465-217A-98	Sequence 98, Appl
24	35	100.0	7	2	US-08-464-329A-98	Sequence 98, Appl
25	35	100.0	7	2	US-08-462-507A-98	Sequence 98, Appl
26	35	100.0	7	2	US-08-776-585-17	Sequence 17, Appl
27	35	100.0	7	2	US-08-467-881A-98	Sequence 98, Appl

28	35	100.0	12	1	US-08-073-028-51	Sequence 51, Appl
29	35	100.0	12	3	US-09-071-877-15	Sequence 15, Appl
30	35	100.0	12	4	US-08-554-616-51	Sequence 51, Appl
31	35	100.0	12	4	US-09-082-279B-219	Sequence 219, App
32	35	100.0	12	4	US-09-045-920-15	Sequence 15, Appl
33	35	100.0	12	4	US-08-474-349A-434	Sequence 434, App
34	35	100.0	12	4	US-09-315-304B-219	Sequence 219, App
35	35	100.0	13	1	US-08-073-028-52	Sequence 52, Appl
36	35	100.0	13	2	US-08-975-699-13	Sequence 13, Appl
37	35	100.0	13	2	US-08-972-089-13	Sequence 13, Appl
38	35	100.0	13	3	US-08-486-099-169	Sequence 169, App
39	35	100.0	13	3	US-08-486-099-170	Sequence 170, App
40	35	100.0	13	3	US-08-486-099-171	Sequence 171, App
41	35	100.0	13	3	US-08-486-099-172	Sequence 172, App
42	35	100.0	13	3	US-08-486-099-173	Sequence 173, App
43	35	100.0	13	3	US-09-071-877-16	Sequence 16, Appl
44	35	100.0	13	3	US-08-484-223B-169	Sequence 169, App
45	35	100.0	13	3	US-08-484-223B-170	Sequence 170, App

ALIGNMENTS

RESULT 1
US-08-257-528B-69
Sequence 69, Application US/08257528B
Patent No. 5639854
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pete
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-257-528B-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 1 ELDKWA 6

RESULT 2
US-08-361-479-1
Sequence 1, Application US/08361479
Patent No. 5693752
GENERAL INFORMATION:
APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,
APPLICANT: GOTTFRIED, MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAIWAL
APPLICANT: GORG, STEINDL, FRANZ
TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH
TITLE OF INVENTION: NEUTRALIZE GENETICALLY DIVERGENT HIV-1 ISOLATES.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,479
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/932,787
FILING DATE: 29-AUG-1992
APPLICATION NUMBER: A 987/92
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 366.015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HIV-1
STRAIN:
INDIVIDUAL ISOLATE: BH10
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: GP160 FRAGMENT
LOCATION: RESIDUE 662 TO 667
IDENTIFICATION METHOD:
OTHER INFORMATION: EPTIPE OF HUMAN MONOCLONAL ANTIBODY
OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-361-479-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
|||||
DB 1 ELDKWA 6

RESULT 3
US-08-473-576-1
Sequence 1, Application US/08473576
Patent No. 5756674
GENERAL INFORMATION:
APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,
APPLICANT: GOTTFRIED, MUSTER, THOMAS; TRKOLA, ALEXANDRA; PURTSCHER, MARTIN; MAI
APPLICANT: GORG, STEINDL, FRANZ
TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH
TITLE OF INVENTION: NEUTRALIZE GENETICALLY DIVERGENT HIV-1 ISOLATES.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,576
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/361,479
FILING DATE: 22-DEC-1994
APPLICATION NUMBER: 07/932,787
FILING DATE: 29-AUG-1992
APPLICATION NUMBER: A 987/92
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 366.015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HIV-1
STRAIN:
INDIVIDUAL ISOLATE: BH10
DEVELOPMENTAL STAGE:
HAPOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: GP160 FRAGMENT
LOCATION: RESIDUE 662 TO 667
IDENTIFICATION METHOD:
OTHER INFORMATION: EPTIPE OF HUMAN MONOCLONAL ANTIBODY
OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-473-576-1

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKMA 6
|||||
Db 1 ELDKMA 6

RESULT 4
US-08-460-602A-69
; Sequence 69, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,602A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-460-602A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKMA 6
|||||
Db 1 ELDKMA 6

RESULT 5
US-08-323-192D-47
; Sequence 47, Application US/08323192D
; Patent No. 5786199
; GENERAL INFORMATION:
; APPLICANT: Palese, Peter
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
; TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,192D
; FILING DATE: 14-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7682-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-323-192D-47

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKMA 6
|||||
Db 1 ELDKMA 6

RESULT 6
US-08-463-966A-69
; Sequence 69, Application US/08463966A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,966A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 1 ELDKWA 6

RESULT 7
US-08-465-217A-69
Sequence 69, Application US/08465217A
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
US-08-465-217A-69

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 1 ELDKWA 6

RESULT 8
US-08-464-329A-69
Sequence 69, Application US/08464329A
Patent No. 5817754
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-69

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 1 ELDKWA 6

RESULT 9
US-08-021-879-1
Sequence 1, Application US/08021879

Patent No. 5817767
GENERAL INFORMATION:
APPLICANT: Graham P. Allaway
TITLE OF INVENTION: SYNERGISTIC COMPOSITION OF CD4-BASED
TITLE OF INVENTION: PROTEIN AND ANTI-HIV-1 ANTIBODY, AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,879
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41189/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 COOPUT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-021-879-1
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 10
US-08-470-887A-46
Sequence 46, Application US/08470887A
Patent No. 5820871
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,887A

FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-470-887A-46
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
Db 1 ELDKWA 6
RESULT 11
US-08-252-508B-46
Sequence 46, Application US/08252508B
Patent No. 5854037
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXPRESSION SYSTEMS AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,508B
FILING DATE: 01-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-252-508B-46
Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 12

US-08-975-699-23
; Sequence 23, Application US/08975699
; Patent No. 5858369

GENERAL INFORMATION:

APPLICANT: MATSUO, KAZUHIRO
APPLICANT: CHUJO, YOSHITOMO
APPLICANT: YAMAZAKI, AKIHIRO
APPLICANT: HONDA, MITSUO
APPLICANT: YAMAKAZI, SHUDO
APPLICANT: TASAKI, HIROMICHI
TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
TITLE OF INVENTION: VACCINE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,699
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/619,512
FILING DATE: 29-MAR-1996
APPLICATION NUMBER: PCT/JP95/01515
FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 178462/1994
FILING DATE: 29-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-795-0X PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
STRAIN: HIV-1

US-08-975-699-23

Query Match

Best Local Similarity 100.0%; Score 35; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 13

US-08-417-210A-147
; Sequence 147, Application US/08417210A
; Patent No. 5863542

GENERAL INFORMATION:

APPLICANT: PAOLETTI, ENZO
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXYRUS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,210A
FILING DATE: 05-APR-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOMALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2690
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-840-3333

INFORMATION FOR SEQ ID NO: 147:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: amino acid

US-08-417-210A-147

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

RESULT 14

US-08-843-718-1
; Sequence 1, Application US/08843718
; Patent No. 5866694

GENERAL INFORMATION:

APPLICANT: KATINGER, HERMAN; RUEKER, FLORIAN; HIMMLER,
APPLICANT: GOTTFRIED; MUSTER, THOMAS; TRKOJA, ALEXANDRA; PURTSCHER, MARTIN; MAI
APPLICANT: GEORG; STEINDL, FRANZ
TITLE OF INVENTION: PEPTIDES THAT INDUCE ANTIBODIES WHICH
TITLE OF INVENTION: NEUTRALIZE GENETICALLY DIVERGENT HIV-1 ISOLATES.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

Qy 1 ELDKWA 6
|||||
Db 1 ELDKWA 6

SOFTWARE: WORDPERECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,718
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/932,787
FILING DATE: 29-AUG-1992
APPLICATION NUMBER: A 987/92
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSELLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 366,015
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HIV-1
STRAIN:
INDIVIDUAL ISOLATE: BH10
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY: GP160 FRAGMENT
LOCATION: RESIDUE 662 TO 667
IDENTIFICATION METHOD:
OTHER INFORMATION: EPTOPE OF HUMAN MONOCLONAL ANTIBODY
OTHER INFORMATION: DIRECTED AGAINST HIV-1 GP160
US-08-843-718-1

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 1 ELDKWA 6

RESULT 15
US-08-462-507A-69
Sequence 69, Application US/08462507A
Patent No. 5876731
GENERAL INFORMATION:
APPLICANT: STA, Charles D. Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-69

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELDKWA 6
DB 1 ELDKWA 6

Search completed: May 7, 2003, 09:59:51
Job time: 2.77778 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 3.30556 Seconds
(without alignments)
167.038 Million cell updates/sec

Title: US-09-877-606-6

Perfect score: 35

Sequence: 1 ELDKWA 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PC1_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	6	10	US-09-873-459A-4
2	35	100.0	7	10	US-09-873-459A-2
3	35	100.0	10	9	US-09-931-325A-132
4	35	100.0	14	9	US-09-931-325A-133
5	35	100.0	15	10	US-09-810-310-41
6	35	100.0	36	9	US-09-874-475-16
7	35	100.0	36	9	US-10-116-797-1
8	35	100.0	36	9	US-09-493-346-1
9	35	100.0	36	10	US-09-796-202-10
10	35	100.0	36	10	US-09-779-451-5
11	35	100.0	36	10	US-09-779-451-47
12	35	100.0	36	10	US-08-779-451-50
13	35	100.0	36	10	US-09-779-451-56
14	35	100.0	36	10	US-09-912-824-1
15	35	100.0	36	10	US-09-834-628-1
16	35	100.0	36	10	US-09-854-816-1
17	35	100.0	36	10	US-09-854-816-108
18	35	100.0	37	9	US-09-848-616-176
19	35	100.0	40	10	US-09-854-816-113

20	35	100.0	46	10	US-09-779-451-41	Sequence 41, Appl
21	35	100.0	46	10	US-09-779-451-45	Sequence 45, Appl
22	35	100.0	46	10	US-09-779-451-48	Sequence 48, Appl
23	35	100.0	46	10	US-09-779-451-54	Sequence 54, Appl
24	35	100.0	46	10	US-09-854-816-109	Sequence 109, App
25	35	100.0	46	10	US-09-854-816-112	Sequence 112, App
26	35	100.0	56	10	US-09-779-451-4	Sequence 4, Appl1
27	35	100.0	145	12	US-10-000-321-11	Sequence 11, Appl1
28	35	100.0	177	9	US-10-040-349B-2	Sequence 2, Appl1
29	35	100.0	189	10	US-09-854-816-100	Sequence 100, App
30	35	100.0	198	10	US-09-854-816-86	Sequence 86, Appl
31	35	100.0	198	10	US-09-854-816-87	Sequence 87, Appl
32	35	100.0	198	10	US-09-854-816-88	Sequence 88, Appl
33	35	100.0	198	10	US-09-854-816-89	Sequence 89, Appl
34	35	100.0	198	10	US-09-854-816-90	Sequence 90, Appl
35	35	100.0	198	10	US-09-854-816-97	Sequence 97, Appl
36	35	100.0	198	10	US-09-854-816-99	Sequence 99, Appl
37	35	100.0	198	10	US-09-854-816-101	Sequence 101, App
38	35	100.0	221	9	US-10-059-271-84	Sequence 84, Appl
39	35	100.0	232	9	US-10-059-271-81	Sequence 81, Appl
40	35	100.0	233	10	US-09-854-816-49	Sequence 49, Appl
41	35	100.0	233	10	US-09-854-816-50	Sequence 50, Appl
42	35	100.0	254	9	US-10-059-271-82	Sequence 82, Appl
43	35	100.0	256	9	US-10-059-271-97	Sequence 97, Appl
44	35	100.0	267	10	US-09-854-816-15	Sequence 15, Appl
45	35	100.0	267	10	US-09-854-816-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-09-873-459A-4
Sequence 4, Application US/09873459A
Patent No. US20020064533A1
GENERAL INFORMATION:
APPLICANT: Murrav, Kenneth
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/110,911
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 6
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-09-873-459A-4
Query Match 100.0%; Score 35; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELDKWA 6
DB 1 ELDKWA 6
RESULT 2
US-09-873-459A-2
Sequence 2, Application US/09873459A
Patent No. US20020064533A1
GENERAL INFORMATION:
APPLICANT: Murrav, Kenneth
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A

;; CURRENT FILING DATE: 2001-09-17
;; PRIOR APPLICATION NUMBER: PCT/US99/28755
;; PRIOR FILING DATE: 1999-12-03
;; PRIOR APPLICATION NUMBER: 60/110,911
;; PRIOR FILING DATE: 1998-12-04
;; NUMBER OF SEQ ID NOS: 47
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 2
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Human immunodeficiency virus
US-09-873-459A-2

Query Match 100.0%; Score 35; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 1 ELDKWA 6

RESULT 3
US-09-931-325A-132
;; Sequence 132, Application US/09931325A
;; Publication No. US20030054337A1
;; GENERAL INFORMATION:
;; APPLICANT: Birkett, Ashley J.
;; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
;; FILE REFERENCE: 4564/83503 ICC-103.1
;; CURRENT APPLICATION NUMBER: US/09/931,325A
;; CURRENT FILING DATE: 2002-02-22
;; PRIOR APPLICATION NUMBER: 60/225,843
;; PRIOR FILING DATE: 2000-08-16
;; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGND
;; PRIOR FILING DATE: 2001-08-15
;; NUMBER OF SEQ ID NOS: 186
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 132
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Human immunodeficiency virus type 1
US-09-931-325A-132

Query Match 100.0%; Score 35; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 3 ELDKWA 8

RESULT 4
US-09-931-325A-133
;; Sequence 133, Application US/09931325A
;; Publication No. US20030054337A1
;; GENERAL INFORMATION:
;; APPLICANT: Birkett, Ashley J.
;; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
;; FILE REFERENCE: 4564/83503 ICC-103.1
;; CURRENT APPLICATION NUMBER: US/09/931,325A
;; CURRENT FILING DATE: 2002-02-22
;; PRIOR APPLICATION NUMBER: 60/225,843
;; PRIOR FILING DATE: 2000-08-16
;; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGND
;; PRIOR FILING DATE: 2001-08-15
;; NUMBER OF SEQ ID NOS: 186
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 133
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Human immunodeficiency virus type 1

US-09-931-325A-133

Query Match 100.0%; Score 35; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 6 ELDKWA 11

RESULT 5
US-09-810-310-41
;; Sequence 41, Application US/09810310
;; Patent No. US20020044948A1
;; GENERAL INFORMATION:
;; APPLICANT: Khleif, Samir N.
;; APPLICANT: Berzofsky, Jay A.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
;; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
;; FILE REFERENCE: 15280-41510005
;; CURRENT APPLICATION NUMBER: US/09/810,310
;; CURRENT FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/189,396
;; PRIOR FILING DATE: 2000-03-15
;; NUMBER OF SEQ ID NOS: 61
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 41
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
US-09-810-310-41

Query Match 100.0%; Score 35; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 6 ELDKWA 11

RESULT 6
US-09-874-475-16
;; Sequence 16, Application US/09874475
;; Publication No. US20020182592A1
;; GENERAL INFORMATION:
;; APPLICANT: Petropoulos, Christos J.
;; APPLICANT: Parkin, Neil T.
;; APPLICANT: Whitcomb, Jeanette
;; APPLICANT: Huang, Wei
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EVALUATING VIRAL RECEPTOR/CO-RECE
;; TITLE OF INVENTION: AND INHIBITORS OF VIRUS ENTRY USING RECOMBINANT VIRUS ASSAYS
;; FILE REFERENCE: 2793/65166
;; CURRENT APPLICATION NUMBER: US/09/874,475
;; CURRENT FILING DATE: 2001-06-04
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 16
;; LENGTH: 36
;; TYPE: PRT
;; ORGANISM: Fusion Inhibitor Peptide
US-09-874-475-16

Query Match 100.0%; Score 35; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||

Db 25 ELDKWA 30

```
RESULT 7
US-10-116-797-1
; Sequence 1, Application US/10116797
; Publication No. US20030044411A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, William C.
; APPLICANT: Maddon, Paul J.
; TITLE OF INVENTION: METHODS FOR INHIBITING HIV-1 INFECTION
; FILE REFERENCE: 64672-A
; CURRENT APPLICATION NUMBER: US/10/116,797
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-797-1
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Query Match 100.0%; Score 35; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
Db 25 ELDKWA 30

```
RESULT 8
US-09-493-346-1
; Sequence 1, Application US/09493346
; Publication No. US20030082185A1
; GENERAL INFORMATION:
; APPLICANT: Olson, William C
; APPLICANT: Maddon, Paul J
; TITLE OF INVENTION: Compositions and Methods for Inhibition of HIV-1
; FILE REFERENCE: 61009
; CURRENT APPLICATION NUMBER: US/09/493,346
; CURRENT FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T20 peptide
US-09-493-346-1
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Query Match 100.0%; Score 35; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
Db 25 ELDKWA 30

```
RESULT 9
US-09-796-202-10
; Sequence 10, Application US/09796202
; Patent No. US2002006813A1
; GENERAL INFORMATION:
; APPLICANT: Dragic, Tatjana
; APPLICANT: Olson, William
; TITLE OF INVENTION: SULFATED CCR5 PEPTIDES FOR HIV-1 INFECTION
; FILE REFERENCE: 2048/61010/JPM/SHS
; CURRENT APPLICATION NUMBER: US/09/796,202
; CURRENT FILING DATE: 2001-02-28
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; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 36
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: T-20
US-09-796-202-10
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Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
Db 25 ELDKWA 30

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RESULT 10
US-09-779-451-5
; Sequence 5, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-5
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Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
Db 25 ELDKWA 30

```
RESULT 11
US-09-779-451-47
; Sequence 47, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 36
; TYPE: PRT
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; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-47

Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 25 ELDKWA 30

RESULT 12
US-09-779-451-50
; Sequence 50, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:

; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 50
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human Immunodeficiency virus type 1
US-09-779-451-50

Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 25 ELDKWA 30

RESULT 13
US-09-779-451-56
; Sequence 56, Application US/09779451
; Patent No. US20020094521A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 56
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human Immunodeficiency virus type 1
US-09-779-451-56

Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||

DB 25 ELDKWA 30

RESULT 14
US-09-912-824-1
; Sequence 1, Application US/09912824
; Patent No. US20020106374A1
; GENERAL INFORMATION:

; APPLICANT: Progenics Pharmaceuticals, Inc.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF HIV-1 INFECTION
; FILE REFERENCE: 2048/62942-B
; CURRENT APPLICATION NUMBER: US/09/912,824
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T20 Peptide
US-09-912-824-1

Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 25 ELDKWA 30

RESULT 15
US-09-834-628-1
; Sequence 1, Application US/09834628
; Patent No. US20020119922A1
; GENERAL INFORMATION:
; APPLICANT: YU, YEON-GYU
; APPLICANT: KIM, KEY-SUN
; APPLICANT: JIN, BONG-SUK
; TITLE OF INVENTION: PEPTIDES FOR INHIBITION OF HIV INFECTION
; FILE REFERENCE: 05823.0198-00000
; CURRENT APPLICATION NUMBER: US/09/834,628
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: KR 00-65664
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Dp178
US-09-834-628-1

Query Match 100.0%; Score 35; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ELDKWA 6
|||||
DB 25 ELDKWA 30

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:40:21 ; Search time 6.38426 Seconds

(without alignments)
146.102 Million cell updates/sec

Title: US-09-877-606-7

Perfect score: 48

Sequence: 1 LMNPNFNT 7

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Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	48	100.0	15 10 AAP90238	Antigenic peptide
2	48	100.0	15 22 AAU12524	Human HIV-1 Th-CTL
3	48	100.0	15 22 AAU12532	Human HIV-1 Th-CTL
4	48	100.0	15 22 AAU12542	Human HIV-1 Th-CTL
5	48	100.0	20 17 AAU07920	gp41 peptide 53.
6	48	100.0	23 9 AAP82469	Peptide component
7	48	100.0	23 17 AAU07974	HIV peptide 41-21.
8	48	100.0	23 22 AAU12483	HIV Th-CTL peptide
9	48	100.0	24 22 AAU12488	HIV Th-CTL peptide
10	48	100.0	24 23 AAU70251	HIV Th-CTL p17 epi

11	48	100.0	32 22 AAU12479	HIV Th-CTL peptide
12	48	100.0	32 23 AAU070242	HIV Th-CTL overlap
13	48	100.0	33 23 ABB09199	HIV-1 gp160 amino
14	48	100.0	36 21 AAU17022	DP-178-derived pep
15	48	100.0	36 21 AAY89188	Core polypeptide f
16	48	100.0	36 21 AAY89189	Core polypeptide f
17	48	100.0	36 21 AAY89190	Core polypeptide f
18	48	100.0	36 21 AAY89191	Core polypeptide f
19	48	100.0	36 21 AAY89193	Core polypeptide f
20	48	100.0	36 21 AAY89194	Core polypeptide f
21	48	100.0	36 21 AAY89195	Core polypeptide f
22	48	100.0	36 21 AAY89197	Core polypeptide f
23	48	100.0	36 21 AAY89199	Core polypeptide f
24	48	100.0	36 21 AAY89200	Core polypeptide f
25	48	100.0	36 21 AAY89200	Core polypeptide f
26	48	100.0	36 22 ABB00546	Core polypeptide f
27	48	100.0	36 22 ABB00547	Viral DP178/107-11
28	48	100.0	36 22 ABB00548	Viral DP178/107-11
29	48	100.0	36 22 ABB00549	Viral DP178/107-11
30	48	100.0	36 22 ABB00550	Viral DP178/107-11
31	48	100.0	36 22 ABB00551	Viral DP178/107-11
32	48	100.0	36 22 ABB00552	Viral DP178/107-11
33	48	100.0	36 22 ABB00553	Viral DP178/107-11
34	48	100.0	36 22 ABB00554	Viral DP178/107-11
35	48	100.0	36 22 ABB00555	Viral DP178/107-11
36	48	100.0	36 22 ABB00556	Viral DP178/107-11
37	48	100.0	36 22 ABB00557	Viral DP178/107-11
38	48	100.0	36 22 ABB00558	Viral DP178/107-11
39	48	100.0	36 22 ABB00559	Viral DP178/107-11
40	48	100.0	36 22 ABB00560	Viral DP178/107-11
41	48	100.0	36 22 ABB00561	Viral DP178/107-11
42	48	100.0	36 22 ABB00562	Viral DP178/107-11
43	48	100.0	36 22 ABB00563	Viral DP178/107-11
44	48	100.0	36 22 ABB00564	Viral DP178/107-11
45	48	100.0	36 22 ABB00565	Viral DP178/107-11

ALIGNMENTS

RESULT 1
ID AAP90238 standard; peptide; 15 AA.
XX AAP90238;
AC 26-FEB-1990 (first entry)
XX
DT
XX Antigenic peptide for detecting, inhibiting and neutralising HIV-1.
DE HIV-1; antigenic determinants.
XX
KW
XX
OS HIV-1.
XX
PN EP330359-A.
XX
PD 30-AUG-1989.
XX
PF 14-FEB-1989; 89EP-0301364.
XX
PR 25-FEB-1988; 88US-0160378.
XX
PA (BIRA) BIO RAD LABS INC.
XX
PI Walker RP, Parekh BS;
XX
DR WPI: 1989-250452/35.
XX
PT New peptide(s) for detecting, inhibiting and neutralising HIV-1
PT corresp. to antigenic determinants encoded by conserved regions
PT of HIV-1 genome.
PS Disclosure: page 4; 16pp; English.

XX Peptide is one of several fragments from gp 120 and gp41 (env gene)
CC p18 and p24 (gag gene), p32 (pol gene) and proteins encoded by the
CC tat, rev, trs/art and sor genes. They are used for detecting,
CC inhibiting and neutralising HIV-1 infection. Dosage is pref.
CC 5-25 mg/kg. The peptides can be used for any type of immunological
CC detection esp. dot blot and ELISA.
CC See also AAP90191-P90274.
XX
SQ Sequence 15 AA:
Query Match 100.0%; Score 48; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMFNI 7
| | | | |
DB 9 LMNMFNI 15
RESULT 2
AAU12524
ID AAU12524 standard; Peptide: 15 AA.
XX
AC AAU12524;
XX
DT 27-SEP-2001 (first entry)
XX
DE Human HIV-1 Th-CTL overlapping epitope #31.
XX
KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
KW Vaccinia ankara.
XX
OS Homo sapiens.
OS Human immunodeficiency virus type 1.
XX
PN WO200156355-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03540.
XX
PR 04-FEB-2000; 2000US-0497497.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Liao H;
XX
DR WPI: 2001-488827/53.
XX
PT Vaccine for immunizing against human immunodeficiency virus has mixture
PT or linear array of peptides comprising immunodominant T-helper epitopes
PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes -
XX
PS Claim 1; Page 26; 33pp; English.
XX
XX The present invention relates to human immunodeficiency virus (HIV)
CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.
CC The vaccine comprises a mixture or linear array of peptides, or its
CC variants, where the peptides contain immunodominant T-helper (Th)
CC epitopes and major histocompatibility complex (MHC) cytotoxic T-
CC lymphocyte (CTL) epitopes and the linear array of peptides are
CC preferably expressed in modified Vaccinia ankara. The vaccine is useful
CC for immunising a patient against HIV and focuses immune response on many
CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with
CC linear arrays of CTL epitopes can be used as either primes or boosts of
CC peptides or of each other to optimally give CTL anti-HIV responses. The
CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558
CC represent the amino acid sequences of the Th-CTL epitopes and HIV
CC immunogenic peptides used in the invention.

SQ Sequence 15 AA:
Query Match 100.0%; Score 48; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMFNI 7
| | | | |
DB 3 LMNMFNI 9
RESULT 3
AAU12532
ID AAU12532 standard; Peptide: 15 AA.
XX
AC AAU12532;
XX
DT 27-SEP-2001 (first entry)
XX
DE Human HIV-1 Th-CTL overlapping epitope #39.
XX
KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
KW Vaccinia ankara.
XX
OS Homo sapiens.
OS Human immunodeficiency virus type 1.
XX
PN WO200156355-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03540.
XX
PR 04-FEB-2000; 2000US-0497497.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Liao H;
XX
DR WPI: 2001-488827/53.
XX
PT Vaccine for immunizing against human immunodeficiency virus has mixture
PT or linear array of peptides comprising immunodominant T-helper epitopes
PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes -
XX
PS Disclosure; Page 27; 33pp; English.
XX
XX The present invention relates to human immunodeficiency virus (HIV)
CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.
CC The vaccine comprises a mixture or linear array of peptides, or its
CC variants, where the peptides contain immunodominant T-helper (Th)
CC epitopes and major histocompatibility complex (MHC) cytotoxic T-
CC lymphocyte (CTL) epitopes and the linear array of peptides are
CC preferably expressed in modified Vaccinia ankara. The vaccine is useful
CC for immunising a patient against HIV and focuses immune response on many
CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with
CC linear arrays of CTL epitopes can be used as either primes or boosts of
CC peptides or of each other to optimally give CTL anti-HIV responses. The
CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558
CC represent the amino acid sequences of the Th-CTL epitopes and HIV
CC immunogenic peptides used in the invention.

SQ Sequence 15 AA:
Query Match 100.0%; Score 48; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMFNI 7
| | | | |
DB 3 LMNMFNI 9

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RESULT 4
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ID AAU12542 standard; Peptide; 15 AA.
XX
AC AAU12542;
XX
DT 27-SEP-2001 (first entry)
XX
DE Human HIV-1 Th-CTL overlapping epitope #49.
XX
KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
KM human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
XX
OS Homo sapiens.
XX Human immunodeficiency virus type 1.
XX
PN WO200156355-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03540.
XX
PR 04-FEB-2000; 2000US-0497497.
XX
PA (UYDG-) UNIV DUKE.
XX
PI Haynes BF, Liao H;
XX
DR WPI; 2001-488827/53.
XX
PT Vaccine for immunizing against human immunodeficiency virus has mixture
PT or linear array of peptides comprising immunodominant T-helper epitopes
PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes
XX
PS Disclosure; Page 27; 33pp; English.
XX
CC The present invention relates to human immunodeficiency virus (HIV)
CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.
CC The vaccine comprises a mixture or linear array of peptides, or its
CC variants, where the peptides contain immunodominant T-helper (Th)
CC epitopes and major histocompatibility complex (MHC) cytotoxic T-
CC lymphocyte (CTL) epitopes and the linear array of peptides are
CC preferably expressed in modified Vaccinia ankara. The vaccine is useful
CC for immunising a patient against HIV and focuses immune response on many
CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with
CC linear arrays of CTL epitopes can be used as either primes or boosts of
CC peptides or of each other to optimally give CTL anti-HIV responses. The
CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558
CC represent the amino acid sequences of the Th-CTL epitopes and HIV
CC immunogenic peptides used in the invention.
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 48; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMENI 7
DB 3 LMNMENI 9
RESULT 5
AAW07920
ID AAW07920 standard; peptide; 20 AA.
XX
AC AAW07920;
XX
DT 31-JAN-1997 (first entry)

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XX
DE gp41 peptide 53.
XX
KM HIV; gp120; HIV-IIIB strain; HIV-1 transmission; foetal transmission;
KM neutralising antibody; passive immunisation; anti-idiotypic antibody;
XX
KW gp41; vaccine; active immunotherapy.
XX
OS Human immunodeficiency virus type 1.
XX
PN US5556744-A.
XX
PD 17-SEP-1996.
XX
PF 24-MAR-1994; 94US-0218025.
XX
PR 24-MAR-1994; 94US-0218025.
XX
PR 29-MAY-1992; 92US-0891451.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
PI Ugen KE, Weiner DB, Williams WV;
XX
DR WPI; 1996-432980/43.
XX
PT Determining the likelihood of maternal transmission of HIV-1 to
PT foetus - by measuring maternal reactivity with specific gp120 and
PT gp41 derived peptide(s), also used for diagnosing HIV in infants
XX
PS Claim 1; Column 115; 63pp; English.
XX
CC AAW07918-W07928 represent HIV gp41 peptides that can be used in the
CC method of the invention. These sequences are derived from the HIV-IIIB
CC strain deposited as ATCC CRL 8543. The method of the invention is for
CC determining whether or not a mother will transmit HIV-1 to a foetus.
CC The method comprises incubating a sample from the HIV-infected mother,
CC with a collection of HIV peptides. The HIV peptides includes at least
CC one of these sequences, and at least one HIV gp120 derived peptide (see
CC AAW07909-W07917). The number of peptides that react with the sample is
CC determined, and this number is compared with a standard that shows
CC pattern reactivity for a patient of transmission status. A
CC non-transmissible HIV sample is indicated if the test sample reacts with
CC twice as many peptides as the standard. The method detects the presence
CC of neutralising antibodies that protect against mother to infant
CC transmission of HIV. These sequences can also be used in vaccines to
CC protect against transmission. Antibodies against these sequences can be
CC used for passive immunisation, and to generate anti-idiotypic antibodies
CC for use in vaccines or active immunotherapy.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 48; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMNMENI 7
DB 8 LMNMENI 14
RESULT 6
AAP82469
ID AAP82469 standard; protein; 23 AA.
XX
AC AAP82469;
XX
DT 12-NOV-1990 (first entry)
XX
DE Peptide component of AIDS vaccine.
XX
KM AIDS vaccine; T-cells.
XX
OS synthetic.

```

XX EP273716-A.
 PN 06-JUL-1988.
 PD 23-DEC-1987; 87EP-0311391.
 PF 12-FEB-1987; 87US-0014430.
 PR 30-DEC-1986; 86US-0947935.
 XX (USDC) US SEC OF COMMERCE.
 PA (USSH) US DEPT HEALTH AND HUMAN.
 PI Delisi C, Margalit H, Cornette JL, Ouyang CS;
 DR WPI; 1988-184640/27.
 XX
 PT Synthetic peptide(s) as vaccines for AIDS - selected from peptide
 PT regions which can fold as a maximally amphipathic helix recognised
 PT by T cells.
 XX
 XX Claim 9; Page 10; 16pp; English.
 PS
 CC This peptide is a component of an AIDS vaccine. It can fold as a
 CC maximally amphipathic helix and is recognised by T-cells immune to
 CC the AIDS virus envelope protein.
 CC See also AAP82462-68 and AAP82470-79.
 CC
 XX Sequence 23 AA;
 SQ
 Query Match 100.0%; Score 48; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LMNMFNI 7
 ID |||||
 DB 11 LMNMFNI 17
 RESULT 7
 AAM07974
 ID AAM07974 standard; peptide; 23 AA.
 XX
 AC AAM07974;
 XX
 XX 03-FEB-1997 (first entry)
 DT
 XX
 DE HIV peptide 41-21.
 XX
 KM HIV; gp120; HIV-IIIB strain; HIV-1 transmission; foetal transmission;
 KM neutralising antibody; passive immunisation; anti-idiotypic antibody;
 KM gp41; vaccine; active immunotherapy.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN USS556744-A.
 PD 17-SEP-1996.
 XX
 PF 24-MAR-1994; 94US-0218025.
 XX
 PR 24-MAR-1994; 94US-0218025.
 PR 29-MAY-1992; 92US-0891451.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PI Ugen KE, Weiner DB, Williams WV;
 XX
 DR WPI; 1996-432980/43.
 XX
 PT Determining the likelihood of maternal transmission of HIV-1 to
 PT foetus - by measuring maternal reactivity with specific gp120 and

PT gp41 derived peptide(s), also used for diagnosing HIV in infants
 XX
 PS Example 6; Column 95-96; 63pp; English.
 XX
 CC AAM07956-W07979 represent HIV peptides that can be used in the method
 CC of the invention. The method of the invention is for determining
 CC whether or not a mother will transmit HIV-1 to a foetus. The method
 CC comprises incubating a sample from the HIV-infected mother, with a
 CC collection of HIV peptides. The HIV peptides includes at least one HIV
 CC gp120 derived peptide (see AAM07909-W07917), and at least one HIV gp41
 CC derived peptide (see AAM07918-W07928). The number of peptides that react
 CC with the sample is determined, and this number is compared with a
 CC standard that shows pattern reactivity for a patient of transmission
 CC status. A non-transmissive HIV sample is indicated if the test sample
 CC reacts with twice as many peptides as the standard. The method detects
 CC the presence of neutralising antibodies that protect against mother to
 CC infant transmission of HIV. These sequences can also be used in vaccines
 CC to protect against transmission. Antibodies against these sequences can
 CC be used for passive immunisation, and to generate anti-idiotypic
 CC antibodies for use in vaccines or active immunotherapy.
 CC
 XX Sequence 23 AA;
 SQ
 Query Match 100.0%; Score 48; DB 17; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.62;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LMNMFNI 7
 ID |||||
 DB 9 LMNMFNI 15
 RESULT 8
 AAM12483
 ID AAM12483 standard; peptide; 23 AA.
 XX
 AC AAM12483;
 XX
 XX 27-SEP-2001 (first entry)
 DT
 XX
 DE HIV Th-CTL peptide prototype vaccine immunogen #20.
 XX
 KM Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
 KM human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
 KM major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
 KM Vaccinia ankara.
 XX
 OS Homo sapiens.
 XX
 PN WO200156355-A2.
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US03540.
 XX
 PR 04-FEB-2000; 2000US-0497497.
 XX
 PA (UYDU-) UNIV DUKE.
 PI Haynes BF, Liao H;
 XX
 DR WPI; 2001-48827/53.
 XX
 PT Vaccine for immunizing against human immunodeficiency virus has mixture
 PT of linear array of peptides comprising immunodominant T-helper epitopes
 PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes -
 XX
 PS Claim 1; Page 24; 33pp; English.
 XX
 CC The present invention relates to human immunodeficiency virus (HIV)
 CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.
 CC The vaccine comprises a mixture or linear array of peptides, or its
 CC variants, where the peptides contain immunodominant T-helper (Th)

CC epitopes and major histocompatibility complex (MHC) cytotoxic T-
CC lymphocyte (CTL) epitopes and the linear array of peptides are
CC preferably expressed in modified Vaccinia ankara. The vaccine is useful
CC for immunising a patient against HIV and focuses immune response on many
CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with
CC linear arrays of CTL epitopes can be used as either primes or boosts of
CC peptides or of each other to optimally give CTL anti-HIV responses. The
CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558
CC represent the amino acid sequences of the Th-CTL epitopes and HIV
CC immunogenic peptides used in the invention.

XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 48; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. NO. 0.62;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
| | | | | | |
DB 3 LMNWFNI 9

RESULT 9

AAU12488
ID AAU12488 standard; Peptide: 24 AA.

XX
AC AAU12488;

XX
DT 27-SEP-2001 (first entry)

XX
DE HIV Th-CTL peptide prototype vaccine immunogen #25.

XX
KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;

XX
KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;

XX
KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;

XX
KW Vaccinia ankara.

XX
OS Homo sapiens.

XX
PN WO200156355-A2.

XX
PD 09-AUG-2001.

XX
PF 05-FEB-2001; 2001WO-US03540.

XX
PR 04-FEB-2000; 2000US-0497497.

XX
PA (UYDU-) UNIV DUKE.

XX
PI Haynes BF, Liao H;

XX
DR WPI; 2001-488827/53.

XX
PT Vaccine for immunizing against human immunodeficiency virus has mixture

XX
PT or linear array of peptides comprising immunodominant T-helper epitopes

XX
PS Claim 1; Page 25; 33pp; English.

XX
CC The present invention relates to human immunodeficiency virus (HIV)

XX
CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.

XX
CC The vaccine comprises a mixture or linear array of peptides, or its

XX
CC variants, where the peptides contain immunodominant T-helper (Th)

XX
CC lymphocyte (CTL) epitopes and the linear array of peptides are

XX
CC preferably expressed in modified Vaccinia ankara. The vaccine is useful

XX
CC for immunising a patient against HIV and focuses immune response on many

XX
CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with

XX
CC linear arrays of CTL epitopes can be used as either primes or boosts of

XX
CC peptides or of each other to optimally give CTL anti-HIV responses. The

XX
CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558

XX
CC represent the amino acid sequences of the Th-CTL epitopes and HIV

XX
CC immunogenic peptides used in the invention.

XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 48; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. NO. 0.64;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
| | | | | | |
DB 3 LMNWFNI 9

RESULT 10

AAU70251
ID AAU70251 standard; Peptide: 24 AA.

XX
AC AAU70251;

XX
DT 14-FEB-2002 (first entry)

XX
DE HIV TH-CTL P17 epitopes (A2 variants) prototype vaccine D-TH/L-CTL.

XX
KW HIV; human immunodeficiency virus; AIDS; SIV; anti-HIV; virucide;

XX
KW acquired immunodeficiency syndrome; simian immunodeficiency virus;

XX
KW vaccine; cytotoxic T cell response inducer; Th; human leukocyte antigen;

XX
KW immunodominant T-helper epitope; cytotoxic T lymphocyte; CTL; HLA.

XX
OS Human immunodeficiency virus type 1.

XX
OS Synthetic.

XX
PN US2001036461-A1.

XX
PD 01-NOV-2001.

XX
PF 05-FEB-2001; 2001US-0775805.

XX
PR 04-FEB-2000; 2000US-0497497.

XX
PA (HAYN/) HAYNES B F.

XX
PI (LINO/) LIAO H.

XX
PI Haynes BF, Liao H;

XX
DR WPI; 2002-010132/01.

XX
PT Vaccine containing overlapping Th-cytotoxic T lymphocyte epitopes,

XX
PT useful for protecting against human immune deficiency virus

XX
PS Example 1; Page 6; 11pp; English.

XX
CC The invention relates to a vaccine comprising a mixture, or linear array,

XX
CC of specific peptides that are human immunodeficiency virus (HIV-1) Th

XX
CC (immunodominant T-helper epitope)-cytotoxic T lymphocyte (CTL), or their

XX
CC variants. Peptides are also described which contain SIV (simian

XX
CC immunodeficiency virus) derived epitopes. The vaccine is used to protect

XX
CC against infection by HIV. The vaccines are based on an analysis of HLA

XX
CC (human leukocyte antigen) alleles present in subject populations targeted

XX
CC for vaccination and the commonest variants of HIV in the locality. They

XX
CC contain sufficient immunogenic epitopes to ensure effective presentation

XX
CC by almost all members of the target population. The present sequence is

XX
CC an HIV-1 epitope based prototype vaccine of the invention.

XX
SQ Sequence 24 AA;

Query Match 100.0%; Score 48; DB 23; Length 24;
Best Local Similarity 100.0%; Pred. NO. 0.64;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
| | | | | | |
DB 3 LMNWFNI 9

RESULT 11
AAU12479 ID AAU12479 standard; Peptide: 32 AA.
XX
AC AAU12479;
XX
DT 27-SEP-2001 (first entry)
XX
DE HIV Th-CTL peptide prototype vaccine immunogen #16.
XX
KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
KW vaccinia ankara.
XX
OS Homo sapiens.
XX
PN WO200156355-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US03540.
XX
PR 04-FEB-2000; 2000US-0497497.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Haynes BF, Liao H;
XX
DR WPI; 2001-488827/53.
XX
PT Vaccine for immunizing against human immunodeficiency virus has mixture
PT or linear array of peptides comprising immunodominant T-helper epitopes
PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes
XX
PS Claim 1; Page 24; 33pp; English.
XX
CC The present invention relates to human immunodeficiency virus (HIV)
CC and in particular to a human leukocyte antigen (HLA)-based HIV vaccine.
CC The vaccine comprises a mixture or linear array of peptides, or its
CC variants, where the peptides contain immunodominant T-helper (Th)
CC epitopes and major histocompatibility complex (MHC) cytotoxic T-
CC lymphocyte (CTL) epitopes and the linear array of peptides are
CC preferably expressed in modified Vaccinia ankara. The vaccine is useful
CC for immunizing a patient against HIV and focuses immune response on many
CC dominant and subdominant CTL epitopes of HIV. DNA or live vectors with
CC linear arrays of CTL epitopes can be used as either primes or boosts of
CC peptides or of each other to optimally give CTL anti-HIV responses. The
CC vaccine induces salutary anti-HIV immune responses. AAU12447-AAU12558
CC represent the amino acid sequences of the Th-CTL epitopes and HIV
CC immunogenic peptides used in the invention.
XX
SQ Sequence 32 AA;
XX
Query Match 100.0%; Score 48; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LMNMFNI 7
| | | | |
Db 3 LMNMFNI 9
XX
RESULT 12
AAU70242 ID AAU70242 standard; Peptide: 32 AA.
XX
AC AAU70242;
XX
DT 14-FEB-2002 (first entry)
XX
DE HIV Th-CTL overlapping epitopes prototype vaccine D-TH/D-CTL.
XX

KW HIV; human immunodeficiency virus; AIDS; SIV; anti-HIV; virucide;
KW acquired immunodeficiency syndrome; simian immunodeficiency virus;
KW vaccine; cytotoxic T cell response inducer; Th; human leukocyte antigen;
KW immunodominant T-helper epitope; cytotoxic T lymphocyte; CTL; HLA.
XX
OS Human immunodeficiency virus type 1.
OS Synthetic.
XX
PN US2001036461-A1.
XX
PD 01-NOV-2001.
XX
PF 05-FEB-2001; 2001US-0775805.
XX
PR 04-FEB-2000; 2000US-0497497.
XX
PN (HAYN/) HAYNES B F.
XX
PA (LIAO/) LIAO H.
XX
PI Haynes BF, Liao H;
XX
DR WPI; 2002-010132/01.
XX
PT Vaccine containing overlapping Th-cytotoxic T lymphocyte epitopes,
PT useful for protecting against human immune deficiency virus
XX
PS Claim 1; Page 6; 11pp; English.
XX
CC The invention relates to a vaccine comprising a mixture, or linear array,
CC of specific peptides that are human immunodeficiency virus (HIV-1) Th
CC (immunodominant T-helper epitope)-cytotoxic T lymphocyte (CTL), or their
CC variants. Peptides are also described which contain SIV (simian
CC immunodeficiency virus) derived epitopes. The vaccine is used to protect
CC against infection by HIV. The vaccines are based on an analysis of HLA
CC (human leukocyte antigen) alleles present in subject populations targeted
CC for vaccination and the commonest variants of HIV in the locality. They
CC contain sufficient immunogenic epitopes to ensure effective presentation
CC by almost all members of the target population. The present sequence is
CC an HIV-1 epitope based prototype vaccine of the invention.
XX
SQ Sequence 32 AA;
XX
Query Match 100.0%; Score 48; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LMNMFNI 7
| | | | |
Db 3 LMNMFNI 9
XX
RESULT 13
ABB09199 ID ABB09199 standard; Peptide: 33 AA.
XX
AC ABB09199;
XX
DT 04-JUL-2002 (first entry)
XX
DE HIV-1 gp160 amino acid sequence.
XX
KW HIV-1; human immunodeficiency virus; gp41; virology; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN RU2179980-C2.
XX
PD 27-FEB-2002.
XX
PF 20-MAR-2000; 2000RU-0106709.
XX
PR 20-MAR-2000; 2000RU-0106709.
XX

PA (VECT-) VECTOR VIROLOGY & BIOTECHN RES CENTRE.
 PA (BION-) BIOMEDITSINSKII TSETR NON COMMERCE ORGA.
 XX Tumanova Yu O, Kuvshinov VN, Melamed NV, Ushakova TA;
 PI Masharskii Eh A, Illichev AA, Klimov NA, Kozlov AP, Sandakhchlev LS;
 XX WPI: 2002-302480/34.
 DR
 XX Peptide-stimulator of human immunodeficiency type-1 virus protein gp41
 PT conservative epitope recognized by virus-neutralizing monoclonal
 PT antibody 2f5 (variants)
 PS Disclosure: Fig 3; 6pp; Russian.
 XX
 CC The present invention describes 12 peptide-simulators (ABB09187 to
 CC ABB09198) of HIV-1 (human immunodeficiency virus type 1) protein gp41
 CC conservative epitope prepared by affinity selection from phage peptide
 CC libraries. These peptides differ from the HIV-1 protein gp41 conservative
 CC epitope sequence but retain the ability to bind with the virus-
 CC neutralizing monoclonal antibodies 2f5. The invention also describes a
 CC vaccine against HIV based on the peptides. The peptides can be used in
 CC biotechnology, virology, and vaccines. The present sequence represents
 CC an HIV-1 gp160 amino acid sequence given in the exemplification of the
 CC present invention.
 CC
 SQ Sequence 33 AA;
 Query Match 100.0%; Score 48; DB 23; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.89;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMNMFNI 7
 |||||
 Db 18 LMNMFNI 24
 RESULT 14
 AAW17022
 ID AAW17022 standard; peptide; 36 AA.
 XX
 AC AAW17022;
 XX
 DT 01-JUL-1997 (first entry)
 XX
 DE DP-178-derived peptide, T636, having high antiviral activity.
 XX
 DE HIV: SIV: human; simian immunodeficiency virus; glycoprotein 41;
 KM transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition.
 KM replication; transmission.
 XX
 OS Synthetic.
 XX
 PN WO9640191-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09499.
 XX
 PR 07-JUN-1995; 95US-0481957.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Johnson RM, Lambert DM;
 XX
 DR WPI: 1997-099886/09.
 XX
 PT Compens. contg. DP-178 or DP-107 in combination with other
 PT therapeutic agent - useful for treatment of HIV infection, esp. by
 PT inhibiting replication or transmission of HIV.
 XX
 PS Claim 8; Figure 5A (III-IV); 84pp; English.
 CC AAW17021-W17028 are DP-178-derived peptides that have high antiviral

CC activity. DP-178 is a peptide corresponding to residues 638-673 of HIV
 CC type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its
 CC derivatives/homologues are used in combination with a therapeutic agent,
 CC e.g. a reverse transcriptase, viral protease, cytokine, glycosylation or
 CC viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides
 CC work by inhibiting viral replication or inhibiting transmission. They
 CC may also be used in vaccines for protecting against HIV infection.
 CC
 SQ Sequence 36 AA;
 Query Match 100.0%; Score 48; DB 18; Length 36;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMNMFNI 7
 |||||
 Db 28 LMNMFNI 34
 RESULT 15
 AAY89188
 ID AAY89188 standard; peptide; 36 AA.
 XX
 AC AAY89188;
 XX
 DT 23-MAY-2000 (first entry)
 XX
 DE Core polypeptide fragment T No. 627.
 XX
 DE Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
 KM HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
 KM anti-fusogenic; differentiation factor; interleukin; interferon;
 KM colony stimulating factor; hormone; angiogenic factor.
 XX
 OS Unidentified.
 XX
 PN WO959615-A1.
 XX
 PD 25-NOV-1999.
 XX
 PF 20-MAY-1999; 99WO-US11219.
 XX
 PR 20-MAY-1998; 98US-0082279.
 XX
 PA (TRIM-) TRIMERIS INC.
 XX
 PI Baine S, Guthrie KL, Merutka G, Anver MK, Lambert DM;
 XX
 DR WPI: 2000-136792/12.
 XX
 PT A new hybrid polypeptide with enhanced pharmacokinetic properties
 PT comprises enhancer sequence -
 XX
 PS Disclosure: Page 31; 124pp; English.
 XX
 CC The invention relates to hybrid polypeptides comprising enhancer peptide
 CC sequence linked to core polypeptides. The enhancer polypeptides are
 CC derived from various retroviral envelope (gp41) protein sequences,
 CC especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
 CC pharmacokinetic properties such as increasing the half-life of any core
 CC polypeptide that they are linked to. The core polypeptides are any
 CC polypeptide that may be introduced into a living system and that can
 CC function as a pharmacologically useful peptide for the treatment or
 CC prevention of a disease. The core polypeptides are bioactive peptides
 CC selected from a growth factor, cytokine, differentiation factor,
 CC interleukin, interferon, colony stimulating factor, hormone or
 CC angiogenic factor. The peptides of the invention can be used for
 CC inhibiting viral infection and can be used in anti-viral and
 CC anti-fusogenic treatments. Sequences AAY8651-Y90055 represent core
 CC polypeptide fragments that can be used in the invention. Some sequences
 CC among those indicated also comprise enhancer fragments at terminal ends
 CC and form hybrid polypeptides.

Sequence 36 AA:

Query Match 100.0%; Score 48; DB 21; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
|||||||

DB 19 LMNMFNI 25

Search completed: May 7, 2003, 09:53:55
Job time : 7.38426 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 2.36574 Seconds

(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-7

Perfect score: 48

Sequence: 1 LMNPMNI 7

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	851	2 S33985	env polypeptide -
2	48	100.0	852	1 VCLJBR	envelope polypeptide
3	48	100.0	853	2 S54384	env polypeptide - huma
4	48	100.0	854	2 S13288	env polypeptide pr
5	48	100.0	855	1 VCLJZR	env polypeptide pr
6	48	100.0	856	1 VCLJH3	env polypeptide pr
7	48	100.0	861	1 VCLJLV	env polypeptide pr
8	48	100.0	861	1 VCLJSC	env polypeptide pr
9	43	89.6	136	2 J10266	envelope polypeptide
10	43	89.6	136	2 J10266	envelope polypeptide
11	43	89.6	357	2 S22006	envelope protein g
12	43	89.6	357	2 S22004	envelope protein g
13	43	89.6	357	2 S21996	envelope protein g
14	43	89.6	358	2 S21998	envelope protein g
15	43	89.6	358	2 S22002	envelope protein g
16	43	89.6	358	2 S22000	envelope protein g
17	43	89.6	358	2 S70417	envelope protein g
18	43	89.6	443	2 C41621	env polypeptide P
19	43	89.6	454	2 B41621	env polypeptide D
20	43	89.6	729	1 VCLJXX	env polypeptide pr
21	43	89.6	843	1 H44001	env polypeptide pr
22	43	89.6	846	1 VCLJND	env polypeptide pr
23	43	89.6	847	2 T09448	envelope glycoprotein
24	43	89.6	847	2 S13289	env polypeptide - huma
25	43	89.6	854	1 VCLJST	env polypeptide pr
26	43	89.6	855	1 VCLJAJ	env polypeptide pr
27	43	89.6	856	1 VCLJW	env polypeptide pr
28	43	89.6	856	1 A44963	env polypeptide pr
29	43	89.6	859	1 VCLJMN	env polypeptide pr

30	43	89.6	859	2 T01672	envelope polypeptide
31	43	89.6	861	1 VCLJKB	env polypeptide pr
32	42	87.5	856	1 VCLJBR	env polypeptide pr
33	41	85.4	357	2 S21994	envelope protein g
34	40	83.3	125	2 A11358	protein gp30 (Bact
35	40	83.3	424	2 JCS921	non-selective catl
36	39	81.2	193	2 T28706	GTP-binding protei
37	39	81.2	241	2 S53377	probable membr
38	39	81.2	322	2 T40718	probable transmem
39	39	81.2	371	2 I49698	alpha-1,3-galactos
40	39	81.2	376	2 A56480	N-acetylglucosamin
41	39	81.2	394	2 A34417	alpha-1,3-mannosyl
42	39	81.2	439	2 T50688	proline transport
43	39	81.2	574	2 A42950	cyclomaltoextrin
44	38	79.2	323	2 AD0994	probable membrane
45	38	79.2	398	2 C82362	hem protein VC011

ALIGNMENTS

RESULT 1

S33985
env polypeptide - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C:Accession: S33985
R:Carlton, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: EMBL:211530; NID:960192; PID:CAA7628.1; PID:960199
C:Superfamily: type E retrovirus env polypeptide

Query Match 100.0%; Score 48; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNPMNI 7
|||||||
DB 664 LMNPMNI 670

RESULT 2

VCLJBR
env polypeptide - human immunodeficiency virus type 1 (isolate BR)
N:Alternate names: coat protein gp120; coat protein gp41
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997
C:Accession: A31667
R:Andand, R.; Thayer, R.; Srihivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar
Virology 168, 79-89, 1989
A:Title: Biological and molecular characterization of human immunodeficiency virus (H
A:Reference number: A94389; MUID:89085613; PMID:2789516
A:Accession: A31667
A:Molecule type: DNA
A:Residues: 1-852 <ANA>
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; polypeptide; transmembrane protein
F1-516/Product: coat protein gp120 #status predicted <CPI>
F:517-852/Product: coat protein gp41 #status predicted <CP>

Query Match 100.0%; Score 48; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNPMNI 7
|||||||

Db 665 LMNMFNI 671

RESULT 3

SS4384

envelope polypeptide - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C:Accession: S54384

R:Thompson, T.; Buckler-White, A.J.

A:Reference number: S54377

A:Accession: S54384

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-853 <TRH>

A:Cross-references: EMBL:M2639; NID:g329377; PIDN:AAA45370.1; PID:g329385

C:Keywords: polypeptide

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 853;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7

Db 666 LMNMFNI 672

RESULT 4

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

A:Reference number: S13288; MUID:91045044; PMID:2172833

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polypeptide

Query Match

Best Local Similarity 100.0%; Score 48; DB 2; Length 854;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7

Db 667 LMNMFNI 673

RESULT 5

env polypeptide precursor - human immunodeficiency virus Zr-6

C:Species: human immunodeficiency virus Zr-6

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C:Accession: D26192

R:Stinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu

Gene 52, 71-82, 1987

A:Reference number: A26192; MUID:87248097; PMID:3036660

A:Accession: D26192

A:Molecule type: DNA

A:Residues: 1-855 <SRI>

A:Cross-references: GB:K03458; GB:ML6322; NID:g329398; PIDN:AAA45380.1; PID:g329403

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-855/Product: env polypeptide #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,281,297,333,340,355,386,392,398.

Query Match

Best Local Similarity 100.0%; Score 48; DB 1; Length 855;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7

Db 668 LMNMFNI 674

RESULT 6

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03973

R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starck, B.; Josephs, S.F.; D

berger, J.A.; Papas, T.S.; Ghayab, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.

A:Reference number: A03973

A:Accession: A03973

A:Molecule type: DNA

A:Residues: 1-856 <RAV>

A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326383; PIDN:AAA

C:Genetics:

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-511/Product: exterior membrane glycoprotein #status predicted <TM>

F:512-856/Product: transmembrane glycoprotein #status predicted <EXT>

F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,

F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match

Best Local Similarity 100.0%; Score 48; DB 1; Length 856;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7

Db 669 LMNMFNI 675

RESULT 7

env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03975

R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Cell 40, 9-17, 1985

A:Reference number: A90866; MUID:85099333; PMID:2981635

A:Accession: A03975

A:Molecule type: DNA

A:Residues: 1-861 <MAI>

A:Cross-references: GB:K02013; NID:g326417; PIDN:AAB59751.1; PID:g326424

C:Genetics:

C:Superfamily: type E retrovirus env polypeptide

C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-516/Product: exterior membrane glycoprotein #status predicted <EXT>

F:517-861/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,146,161,165,191,202,239,246,267,281,294,300,337,344,361,391,397,402,413
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predic

Query Match 100.0%; Score 48; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMENI 7
|||||
Db 674 LMNMENI 680

RESULT 8
env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)

N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1990 #sequence, revision 31-Dec-1990 #text, change 16-Feb-1997
R:Guirgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta

A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MID:88219542; PMID:3369091

A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>

C:Genetics: env
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote

F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-661/Product: env polypeptide #status predicted <EPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 100.0%; Score 48; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMENI 7
|||||
Db 674 LMNMENI 680

RESULT 9
env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-2) (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text, change 07-Feb-1997
C:Accession: J02066

R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
submitted to JIPD, October 1991
A:Reference number: J0954

A:Accession: J02066
A:Molecule type: DNA
A:Residues: 1-136 <SHI>

C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 89.6%; Score 43; DB 2; Length 136;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMENI 7
|||||
Db 58 LMNMENI 64

RESULT 10
env polypeptide precursor - human immunodeficiency virus type 1 (strain KB-19p41)
J0954
C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 31-Mar-1992 #sequence, revision 31-Mar-1992 #text, change 07-Feb-1997
C:Accession: J0954
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
submitted to JIPD, October 1991

A:Reference number: J0954
A:Accession: J0954
A:Molecule type: DNA
A:Residues: 1-136 <SHI>

C:Superfamily: type E retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 89.6%; Score 43; DB 2; Length 136;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMENI 7
|||||
Db 58 LMNMENI 64

RESULT 11
env polypeptide precursor - human immunodeficiency virus type 1 (patient 41)

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence, revision 20-Feb-1995 #text, change 26-Aug-1999
C:Accession: S70420; S22006

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Reference number: S70417; MID:92144209; PMID:1736940
A:Accession: S70420
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-357 <ST2>

A:Cross-references: EMBL:X61354; NID:960190; PIDN:CAA43620.1; PID:960191
A:Experimental source: patient L
A:Note: Submitted to the EMBL Data Library, July 1991

C:Superfamily: type E retrovirus env polypeptide

Query Match 89.6%; Score 43; DB 2; Length 357;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMENI 7
|||||
Db 170 LMNMENI 176

RESULT 12
env polypeptide precursor - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 4B
C:Date: 20-Feb-1995 #sequence, revision 20-Feb-1995 #text, change 01-Dec-2000

C:Accession: S22004; S70419
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991

A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S22004

A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: EMBL:X61353; NID:960188; PIDN:CAA43618.1; PID:960189

R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer

A:Accession: S70419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-292, 'X', 294-357 <ST2>

A:Cross-references: EMBL:X61353; NID:960188
C:Superfamily: type E retrovirus env polypeptide

Query Match 89.6%; Score 43; DB 2; Length 357;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
 |||||:|
 DB 170 LMNMFNI 176

RESULT 13

S21996
 A:Envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S70422; S21996
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70422
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-357 <STE2>
 A:Cross-references: EMBL:X61356; NID:660181; PIDN:CAA43624.1; PID:61067129
 A:Note: submitted to the EMBL Data Library, July 1991
 C:Superfamily: type E retrovirus env polyprotein

Query Match 89.6%; Score 43; DB 2; Length 357;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
 |||||:|
 DB 170 LMNMFNI 176

RESULT 14

S21998
 A:Envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: isolate 28
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S21998; S70425
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
 A:Reference number: S21998
 A:Accession: S21998
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STE1>
 A:Cross-references: EMBL:X61359; NID:660182; PIDN:CAA43630.1; PID:660183
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 C:Superfamily: type E retrovirus env polyprotein

Query Match 89.6%; Score 43; DB 2; Length 358;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
 |||||:|
 DB 171 LMNMFNI 177

RESULT 15

S22002
 A:Envelope protein gp120/gp41 - human immunodeficiency virus type 1
 C:Species: human immunodeficiency virus type 1, HIV-1
 A:Variety: isolate 3L
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
 C:Accession: S22002; S70418
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
 A:Reference number: S21990
 A:Accession: S22002
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STE1>
 A:Cross-references: EMBL:X61352; NID:660186; PIDN:CAA43616.1; PID:660187
 R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by polymerase chain reaction
 A:Reference number: S70417; MUID:92144209; PMID:1736940
 A:Accession: S70418
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-333, 'X', 335-358 <STE2>
 A:Cross-references: EMBL:X61352; NID:660186
 C:Superfamily: type E retrovirus env polyprotein

Query Match 89.6%; Score 43; DB 2; Length 358;
 Best Local Similarity 85.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
 |||||:|
 DB 171 LMNMFNI 177

Search completed: May 7, 2003, 09:58:41
 Job time : 3.36574 Secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:44:51 ; Search time 1.23148 Seconds

(without alignments)
235.760 Million cell updates/sec

Title: US-09-877-606-7

Perfect score: 48

Sequence: 1 LMNPFNT 7

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:

112892 seqs, 41476328 residues

112892

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	851	1	ENV_HV1B8
2	48	100.0	852	1	ENV_HV1B8
3	48	100.0	853	1	ENV_HV1B8
4	48	100.0	853	1	ENV_HV1B8
5	48	100.0	855	1	ENV_HV1B8
6	48	100.0	856	1	ENV_HV1B8
7	48	100.0	856	1	ENV_HV1B8
8	48	100.0	856	1	ENV_HV1B8
9	48	100.0	856	1	ENV_HV1B8
10	48	100.0	856	1	ENV_HV1B8
11	48	100.0	861	1	ENV_HV1B8
12	43	89.6	843	1	ENV_HV1B8
13	43	89.6	846	1	ENV_HV1B8
14	43	89.6	847	1	ENV_HV1B8
15	43	89.6	847	1	ENV_HV1B8
16	43	89.6	852	1	ENV_HV1B8
17	43	89.6	853	1	ENV_HV1B8
18	43	89.6	854	1	ENV_HV1B8
19	43	89.6	855	1	ENV_HV1B8
20	43	89.6	855	1	ENV_HV1B8
21	43	89.6	856	1	ENV_HV1B8
22	43	89.6	856	1	ENV_HV1B8
23	43	89.6	859	1	ENV_HV1B8
24	43	89.6	861	1	ENV_HV1B8
25	43	89.6	863	1	ENV_HV1B8
26	43	89.6	865	1	ENV_HV1B8
27	42	87.5	848	1	ENV_HV1B8
28	42	87.5	856	1	ENV_HV1B8
29	42	87.5	867	1	ENV_HV1B8
30	39	81.2	193	1	ENV_HV1B8
31	39	81.2	241	1	ENV_HV1B8
32	39	81.2	394	1	ENV_HV1B8
33	39	81.2	574	1	ENV_HV1B8

34	39	81.2	1028	1	FDXG_HAEIN
35	38	79.2	610	1	NU5M_SQUAC
36	38	79.2	855	1	ENV_HV1B8
37	37	77.1	625	1	TR11_MOUSE
38	36	75.0	207	1	VE39_METUA
39	36	75.0	245	1	TEV1_BPT4
40	36	75.0	366	1	VE59_STAAM
41	36	75.0	401	1	SVY_HAEIN
42	36	75.0	491	1	Y100_YEAST
43	36	75.0	785	1	ISP4_SCHPO
44	35	72.9	289	1	CTR4_SCHPO
45	35	72.9	494	1	CP51_HUMAN

ALIGNMENTS

RESULT 1	ENV_HV1B8	STANDARD:	PRT:	851 AA.
AC	P04582;			
DT	13-AUG-1987 (Rel. 05, Last Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).			
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11684;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511123; PubMed=2578615;			
RA	Ratner L., Haseltine W., Patarca R., Livak K.J., Starck B.R., Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A., Baumanister K., Ivanoff L., Petteway S.R. Jr., Pearson M.T., Lautenberger J.A., Pappas T.S., Ghurayev J., Chang N.T., Gallo R.C., Wong-Staal F.;			
RA	Complete nucleotide sequence of the AIDS virus, HTLV-III.;			
RL	Nature 313:277-284(1985).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	EMBL: K02011; AAA44661.1; -			
DR	HIV: K02011; ENV5B8.			
DR	Glycosylated: P04582; -			
DR	Interpro: IPR000328; Env.GP41.			
DR	Interpro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	506	
FT	CHAIN	507	851	
FT	DISULFID	54	74	
FT	DISULFID	119	205	
FT	DISULFID	126	196	
FT	DISULFID	131	157	
FT	DISULFID	218	247	
FT	DISULFID	228	239	
FT	DISULFID	296	331	
FT	DISULFID	378	440	
FT	DISULFID	385	413	
FT	CARBOHYD	88	88	
FT	CARBOHYD	136	136	
FT	CARBOHYD	141	141	

EXTERIOR MEMBRANE GLYCOPROTEIN.

TRANSMEMBRANE GLYCOPROTEIN.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 851;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
 DB 664 LMNMFNI 670

RESULT 2
 ENV_HV1BN STANDARD; PRT; 852 AA.

AC P12488;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89085613; PubMed=2789516;
 RA Anand R., Thayer R., Srinivasan A., Nayar S., Gardner M., Luciw P., Dandekar S.,
 "Biological and molecular characterization of human immunodeficiency virus (HIV-1) from the brain of a patient with progressive dementia.";
 RT Virology 168:79-89(1989).
 RL -1- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.
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 CC EMBL: M21098; AAA44221.1; -
 DR PIR: A31667; VCLJBR
 DR HIV; M21098; ENV5BRVA.

DR InterPro: IPR000328; ENV_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.

FT CHAIN 1 30
 FT CHAIN 31 507
 FT CHAIN 508 852
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 155
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 330
 FT DISULFID 376 439
 FT DISULFID 383 412
 FT DISULFID 49 49
 FT CARBOHYD 88 88
 FT CARBOHYD 135 135
 FT CARBOHYD 138 138
 FT CARBOHYD 154 154
 FT CARBOHYD 158 158
 FT CARBOHYD 197 197
 FT CARBOHYD 234 234
 FT CARBOHYD 241 241
 FT CARBOHYD 262 262
 FT CARBOHYD 276 276
 FT CARBOHYD 289 289
 FT CARBOHYD 295 295
 FT CARBOHYD 301 301
 FT CARBOHYD 331 331
 FT CARBOHYD 354 354
 FT CARBOHYD 360 360
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 396 396
 FT CARBOHYD 400 400
 FT CARBOHYD 442 442
 FT CARBOHYD 456 456
 FT CARBOHYD 607 607
 FT CARBOHYD 612 612
 FT CARBOHYD 621 621
 FT CARBOHYD 633 633
 FT CARBOHYD 670 670
 FT CARBOHYD 812 812
 SQ SEQUENCE 852 AA; 97203 MW; 2B866345DE915F CRC64;

Query Match 100.0%; Score 48; DB 1; Length 852;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
 DB 665 LMNMFNI 671

RESULT 3
 ENV_HV1MF STANDARD; PRT; 853 AA.

AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.

RX	MEDLINE-90317877; PubMed-1695254.
RA	Stevenson M., Haggerty S., Lamonica C., Mann A.M., Meier C., Wasiak A.: "Cloning and characterization of human immunodeficiency virus type I variants diminished in the ability to induce syncytium-independent cytolysis."; <i>J. Virol.</i> 64:3792-3803(1990).
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CC	-----
DR	EMBL; M33943; AAA44850.1; .
DR	HIV; M33943; ENVSMPA.
DR	InterPro; IPRO00328; Env GP41.
DR	InterPro; IPRO00777; GP120.
DR	Pfam; PF00516; GP120; 1.
DR	Pfam; PF00517; GP41; 1.
KV	AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
FT	SIGNAL. 1 30
FT	CHAIN 31 509
FT	CHAIN 510 853
FT	DISULFID 54 74
FT	DISULFID 119 203
FT	DISULFID 126 194
FT	DISULFID 131 157
FT	DISULFID 216 245
FT	DISULFID 226 237
FT	DISULFID 294 329
FT	DISULFID 376 443
FT	DISULFID 383 416
FT	CARBOHYD 88 88
FT	CARBOHYD 136 136
FT	CARBOHYD 141 141
FT	CARBOHYD 156 156
FT	CARBOHYD 160 160
FT	CARBOHYD 186 186
FT	CARBOHYD 195 195
FT	CARBOHYD 232 232
FT	CARBOHYD 239 239
FT	CARBOHYD 260 260
FT	CARBOHYD 274 274
FT	CARBOHYD 287 287
FT	CARBOHYD 293 293
FT	CARBOHYD 299 299
FT	CARBOHYD 330 330
FT	CARBOHYD 354 354
FT	CARBOHYD 384 384
FT	CARBOHYD 390 390
FT	CARBOHYD 395 395
FT	CARBOHYD 404 404
FT	CARBOHYD 446 446
FT	CARBOHYD 461 461
FT	CARBOHYD 609 609
FT	CARBOHYD 614 614
FT	CARBOHYD 623 623
FT	CARBOHYD 635 635
FT	CARBOHYD 672 672
FT	CARBOHYD 748 748
FT	CARBOHYD 814 814
SO	SEQUENCE 853 AA; 96912 MW; 337B993B6F22ABA CMC64;
QY	Query Match 100.0%; Score 48; DB 1; Length 853; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 LMNPNRI 7

ID	ENV_HV122	STANDARD:	PRF:	853 AA.
DR	01-OCT-1989 (Rel. 12, Created)			
DR	01-OCT-1989 (Rel. 12, Last sequence update)			
DR	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (Z2/CDC-Z34 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11683;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Theodore T. Buckler-White A.			
RL	Submitted (NOV-1988) to the HIV data bank.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: M22639; AAA45370.1; -.			
DR	HIV; M22639; ENV52226.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR000777; GP120.			
DR	Pfam: PF00516; GP120; 1.			
DR	Pfam: PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;			
KW	Signal.			
FT	SIGNAL	1	31	BY SIMILARITY.
FT	CHAIN	32	508	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	509	853	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	206	BY SIMILARITY.
FT	DISULFID	125	197	BY SIMILARITY.
FT	DISULFID	130	154	BY SIMILARITY.
FT	DISULFID	219	248	BY SIMILARITY.
FT	DISULFID	229	240	BY SIMILARITY.
FT	DISULFID	297	330	BY SIMILARITY.
FT	DISULFID	376	442	BY SIMILARITY.
FT	DISULFID	383	415	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	137	137	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	153	153	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	185	185	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	188	188	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	198	198	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	235	235	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	242	242	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	263	263	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	277	277	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	290	290	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	296	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	331	331	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	338	338	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	353	353	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	384	384	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	402	402	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	441	441	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	459	459	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 853 AA: 97043 MW: 849B08CBAFF008 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 853;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
 Db 666 LMNMFNI 672

ENV_HV126 STANDARD; PRT: 855 AA.

AC P04580;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11708;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=87248097; PubMed=3036660;
 RA Srinivasan A., Anand R., Ranganathan P., Feorino P.,
 RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
 RA Sanchez-Pescador R.;
 RT "Molecular characterization of human immunodeficiency virus from
 RT Zaire: nucleotide sequence analysis identifies conserved and variable
 RT domains in the envelope gene."
 RL Gene 52:71-82(1987).

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DR EMBL: K03458; AAA45380.1; -;
 DR PIN; D26192; VCLJZR.
 DR HIV; K03458; ENV526.
 DR InterPro: IPR000328; Env_GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120.1.
 DR Pfam: PF00517; GP41.1.
 KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
 KW signal.
 FT SIGNAL 1 30
 FT CHAIN 511 510 EXTERIOR MEMBRANE GLYCOPROTEIN.
 FT CHAIN 511 855 TRANSMEMBRANE GLYCOPROTEIN.
 FT DISULFID 53 73 BY SIMILARITY.
 FT DISULFID 118 207 BY SIMILARITY.
 FT DISULFID 125 198 BY SIMILARITY.
 FT DISULFID 130 155 BY SIMILARITY.
 FT DISULFID 220 249 BY SIMILARITY.
 FT DISULFID 230 241 BY SIMILARITY.
 FT DISULFID 298 332 BY SIMILARITY.
 FT DISULFID 378 444 BY SIMILARITY.
 FT DISULFID 385 417 BY SIMILARITY.
 FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 264 264 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 404 404 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 447 447 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 464 464 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 610 610 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 673 673 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 855 AA: 96971 MW: 384D3D6E239C3457 CRC64;

Query Match 100.0%; Score 48; DB 1; Length 855;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
 Db 666 LMNMFNI 674

ENV_HV126 STANDARD; PRT: 856 AA.

AC P03575;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope polypeptide precursor [Contains: Exterior membrane glycoprotein (Gp120); Transmembrane glycoprotein (Gp41)].
 GN ENV.

OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11678;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=85111123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
 RA Joseph S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
 RA Baumeister K., Ivanoff L., Petteway S.R., Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III."
 RT Nature 313:277-284(1985).

[2]
 DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N.,
 RA Gregory T.J.;
 RT "Assignment of intrachain disulfide bonds and characterization of
 RT potential glycosylation sites of the type 1 recombinant human
 RT immunodeficiency virus envelope glycoprotein (gp120) expressed in
 RT Chinese hamster ovary cells."
 RT J. Biol. Chem. 265:10373-10382(1990).

Query Match
Best Local Similarity 100.0%; Score 48; DB 1; Length 856;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LMNWENI	7		669	LMNWENI	675
DB	669	LMNWENI	675				
EN	ENV_HV1H3	STANDARD;	PRT;	856	AA.		
AC	P04624;						
DT	13-AUG-1987 (rel. 05, Created)						
DT	01-FEB-1996 (rel. 33, Last sequence update)						
DT	15-JUL-1999 (rel. 38, Last annotation update)						
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].						
GN	ENV.						
OS	Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).						
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.						
OX	NCBI_TaxID=1107;						
RA	SEQUENCE FROM N.A.						
RA	MEDLINE=85282248; PubMed=2988795;						
RA	Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;						
RT	"HIV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";						
RL	Cell 41:979-986(1985).						
CC	-----						
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CC	-----						
DR	EMBL, M14100; AAA44679.1;						
DR	HIV, M14100; ENVSHX83.						
DR	InterPro: IPR000328; Env_GP41.						
DR	InterPro: IPR000777; GP120.						
DR	Pfam: PF00516; GP120.1.						
DR	Pfam: PF00517; GP41.1.						
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.						
FT	SIGNAL	1	30				
FT	CHAIN	511	511				
FT	DISULFID	512	856				
FT	DISULFID	119	205				
FT	DISULFID	126	196				
FT	DISULFID	131	157				
FT	DISULFID	131	157				
FT	DISULFID	218	247				
FT	DISULFID	228	239				
FT	DISULFID	296	331				
FT	DISULFID	378	445				

Query Match
Best Local Similarity 100.0%; Score 48; DB 1; Length 856;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LMNWENI	7		669	LMNWENI	675
DB	669	LMNWENI	675				
EN	ENV_HV1H3	STANDARD;	PRT;	856	AA.		
AC	070626;						
DT	15-JUL-1998 (rel. 36, Last sequence update)						
DT	15-JUL-1999 (rel. 38, Last annotation update)						
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].						
GN	ENV.						
OS	Human immunodeficiency virus type 1 (HIV-1).						
OC	Viruses; Retroviral viruses; Retroviridae; Lentivirus.						
OX	NCBI_TaxID=82834;						
RA	SEQUENCE FROM N.A.						
RA	MEDLINE=95127297; PubMed=7826699;						
RA	Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Bahn B.M., Shaw G.M., Kong L.T., Weiss S.H., Waters D., Gallo R.C., Blattner W.;						
RT	"Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HIV type IIIB)."						
RL	AIDS Res. Hum. Retroviruses 10:1143-1155(1994).						
CC	-----						
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CC	-----						

FT	CARBOHYD	816	816	N-LINKED (GLCNAc. . .) (POTENTIAL).
SO	SEQUENCE	856 AA;	97055 MW;	DARF4D600EB7A08 CRC64;
	Query Match	100.0%	Score 48;	DB 1; Length 856;
	Best Local Similarity	100.0%	Pred. No. 3.5;	
	Matches 7; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
OY	1	LNWFMNI	7	
DB	669	LNWFMNI	675	
	RESULT 11			
ENV_HV1BR		STANDARD;	PRT;	861 AA.
ID	ENV_HV1BR			
AC	P03377;			
DT	21-JUL-1986 (Rel. 01, Last Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
DE	ENV.			
OS	Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11686;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8509933; PubMed=2981635;			
RA	Wain-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;			
RT	"Nucleotide sequence of the AIDS virus, LAV.";			
RU	Cell 40:9-17(1985).			
CC	-----			
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CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; K02013; AAB59751.1; -.			
DR	EMBL; A04321; CAA00352.1; -.			
DR	PIR; A03975; VCLJLV.			
DR	HIV; K02013; ENVSBRU.			
DR	InterPro: IPR000328; Env_GP41.			
DR	InterPro: IPR00777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KM	Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;			
KM	Signal.			
FT	SIGNAL.	1	30	
FT	CHAIN	31	516	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	517	861	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	210	BY SIMILARITY.
FT	DISULFID	126	201	BY SIMILARITY.
FT	DISULFID	131	162	BY SIMILARITY.
FT	DISULFID	223	252	BY SIMILARITY.
FT	DISULFID	233	244	BY SIMILARITY.
FT	DISULFID	301	336	BY SIMILARITY.
FT	DISULFID	383	450	BY SIMILARITY.
FT	DISULFID	390	423	BY SIMILARITY.
FT	CARBOHYD	88		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	136		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	141		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	146		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	161		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	165		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	191		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	202		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	235		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	239		N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	246		N-LINKED (GLCNAc. . .) (POTENTIAL).

FT	CARBOHYD	267	267	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	281	281	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	294	294	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	300	300	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	306	306	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	337	337	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	344	344	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	361	361	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	391	391	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	397	397	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	402	402	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	411	411	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	453	453	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	468	468	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	616	616	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	621	621	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	630	630	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	642	642	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	679	679	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	755	755	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
FT	CARBOHYD	821	821	N-LINKED (GLCNAC . . .)	(POTENTIAL)									
SQ	SEQUENCE	861 AA;	97487 MW;	04DE2B4DAE4FD63A CIGC64;										
<hr/>														
Query Match	Similarity	100.0%	Score 48;	DB 1;	Length 861;									
Best Local	Matches	7;	Conservative	100.0%;	Pred. No. 3.5;									
OY	1 LMNWNENI	7		Mismatches	0; Indels	0; Gaps	0;							
Db	674 LMNWFNI	680												
<hr/>														
RESULT 12														
ENV_HV1Y2	STANDARD:	PRT:	843 AA.											
ID ENV_HV1Y2														
AC P35961;														
DT 01-JUN-1994	(Rel. 29,	Created)												
DT 01-JUN-1994	(Rel. 29,	Last sequence update)												
DT 15-JUL-1994	(Rel. 38,	Last annotation update)												
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].														
GN ENV.														
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).														
OC Viruses: Retroid viruses; Retroviridae; Lentivirus.														
OX NCBI_TaxID=36377;														
RN [1]														
RP SEQUENCE FROM N.A.														
RX MEDLINE=93021387; PubMed=1404605;														
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H., Shaw G.M.;														
RA "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation."														
RL J. Virol. 66:6587-6600(1992).														
CC -----														
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CC CC														
DR EMBL: M93258; NOT_ANNOTATED_CDS.														
DR PIR: HA4001; HA4001.														
DR InterPro: IPR000328; ENV_GP41.														
DR InterPro: IPR000777; GP120.														
DR Pfam: PF00516; GP120; 1.														
DR Pfam: PF00517; GP41; 1.														


```

FT CHAIN 490 843 TRANSMEMBRANE GLYCOPROTEIN.
FT TRANSMEM 738 755 POTENTIAL.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 201 BY SIMILARITY.
FT DISULFID 125 192 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 214 243 BY SIMILARITY.
FT DISULFID 224 235 BY SIMILARITY.
FT DISULFID 326 326 BY SIMILARITY.
FT DISULFID 373 432 BY SIMILARITY.
FT DISULFID 380 405 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 381 381 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 435 435 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 598 598 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 803 803 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 843 AA; 95648 MW; C69DPD971C91871 CRC64;

Query Match 89.6%; Score 43; DB 1; Length 843;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWNT 7
DB 656 LNMWNT 662

RESULT 13
ENV_HVIND STANDARD; PRT; 846 AA.
ID ENV_HVIND
AC P18799;
DT 01-NOV-1990 (Rel. 16, Last Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11695;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90034200; PubMed=2806917;
RA Spire B., Sire J., Zacher V., Rey F., Barre-Sinoussi F., Galibert F.,
RT Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the
RT human immunodeficiency virus.
RL Gene 81:275-284(1989).
CC -1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.

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CC -----
DR EMBL: M27323; AAA44873.1; -
DR PIR: J00066; VCLJND.
DR HTV: M27323; ENVNDK.
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane;
KW Signal.
FT CHAIN 1 29
FT CHAIN 30 501
FT DISULFID 53 73
FT DISULFID 118 200
FT DISULFID 125 191
FT DISULFID 130 152
FT DISULFID 213 242
FT DISULFID 223 234
FT DISULFID 291 328
FT DISULFID 374 435
FT DISULFID 381 408
FT CARBOHYD 87 87
FT CARBOHYD 129 129
FT CARBOHYD 151 151
FT CARBOHYD 179 179
FT CARBOHYD 182 182
FT CARBOHYD 229 229
FT CARBOHYD 236 236
FT CARBOHYD 257 257
FT CARBOHYD 271 271
FT CARBOHYD 284 284
FT CARBOHYD 290 290
FT CARBOHYD 351 351
FT CARBOHYD 382 382
FT CARBOHYD 388 388
FT CARBOHYD 392 392
FT CARBOHYD 395 395
FT CARBOHYD 401 401
FT CARBOHYD 438 438
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FT CARBOHYD 452 452
FT CARBOHYD 601 601
FT CARBOHYD 606 606
FT CARBOHYD 615 615
FT CARBOHYD 627 627
SQ SEQUENCE 846 AA; 96476 MW; 8A3B9DAS27DE2E83 CRC64;

Query Match 89.6%; Score 43; DB 1; Length 846;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWNT 7
DB 659 LNMWNT 665

RESULT 14
ENV_HVIND STANDARD; PRT; 847 AA.
ID ENV_HVIND
AC P19550;
DT 01-FEB-1991 (Rel. 17, Last Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane

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DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses: Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4398(1990).

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DR DR EMBL: M65024; AAA45072.1; -
DR HIV: M8428; ENV5SF162.
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR00777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane;
KV Signal.
FT SIGNAL. 1 29
FT CHAIN 503 847 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 118 203 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 136 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 435 BY SIMILARITY.
FT DISULFID 81 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 847 AA; 96135 MW; 0A901317FD7PF2AB CRC64;
Query Match 89.6%; Score 43; DB 1; Length 847;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

[illegible]

FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA: 96466 MM: CDLE33D73A5BCAE CRC64;

Query Match 89.6%; Score 43; DB 1; Length 847;
Best Local Similarity 85.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
|||||:
Db 660 LMNMFNI 666

Search completed: May 7, 2003, 09:54:39
Job time : 2.23148 secs

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 5.02315 Seconds

(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-7

Perfect score: 48

Sequence: 1 LMNMFNT 7

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:*
2: SP:bacteria:*
3: SP:fungi:*
4: SP:human:*
5: SP:invertebrate:*
6: SP:mammal:*
7: SP:mnc:*
8: SP:organelle:*
9: SP:phage:*
10: SP:plant:*
11: SP:rodent:*
12: SP:virus:*
13: SP:vertebrate:*
14: SP:unclassified:*
15: SP:virus:*
16: SP:bacteriaph:*
17: SP:archaeop:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	117	15	Q9YRT8 human immun
2	48	100.0	117	15	Q9YRT3 human immun
3	48	100.0	117	15	Q9YRS7 human immun
4	48	100.0	117	15	Q9YR6 human immun
5	48	100.0	118	15	Q9E556 human immun
6	48	100.0	118	15	Q9E5R9 human immun
7	48	100.0	118	15	Q9E5R8 human immun
8	48	100.0	118	15	Q9E5G8 human immun
9	48	100.0	118	15	Q9E502 human immun
10	48	100.0	118	15	Q9E5P9 human immun
11	48	100.0	118	15	Q9E5P4 human immun
12	48	100.0	118	15	Q9E5P3 human immun
13	48	100.0	121	15	Q8UQX7 human immun
14	48	100.0	122	15	Q9YXR6 human immun
15	48	100.0	122	15	Q9YXP1 human immun
16	48	100.0	122	15	Q9YXN8 human immun

17	48	100.0	122	15	Q9YXN7 human immun
18	48	100.0	122	15	Q9YXN5 human immun
19	48	100.0	122	15	Q9YXN4 human immun
20	48	100.0	122	15	Q9YXN1 human immun
21	48	100.0	122	15	Q9YXN6 human immun
22	48	100.0	122	15	Q9WR03 human immun
23	48	100.0	122	15	Q9QIW9 human immun
24	48	100.0	122	15	Q9QIW6 human immun
25	48	100.0	122	15	Q9QIW0 human immun
26	48	100.0	122	15	Q9QIU9 human immun
27	48	100.0	122	15	Q9EAA5 human immun
28	48	100.0	122	15	Q9EAA0 human immun
29	48	100.0	122	15	Q9EAA6 human immun
30	48	100.0	122	15	Q9ILK7 human immun
31	48	100.0	122	15	Q9ILK1 human immun
32	48	100.0	122	15	Q9ILK0 human immun
33	48	100.0	122	15	Q9IL07 human immun
34	48	100.0	122	15	Q9ID01 human immun
35	48	100.0	122	15	Q9IDP9 human immun
36	48	100.0	122	15	Q9IDP7 human immun
37	48	100.0	122	15	Q9IDP2 human immun
38	48	100.0	122	15	Q9IDU1 human immun
39	48	100.0	122	15	Q9DPY4 human immun
40	48	100.0	122	15	Q9DPT0 human immun
41	48	100.0	122	15	Q9DSD9 human immun
42	48	100.0	122	15	Q9DDP1 human immun
43	48	100.0	122	15	Q9DDK1 human immun
44	48	100.0	126	15	Q9YXY3 human immun
45	48	100.0	127	15	Q9YX6 human immun

ALIGNMENTS

RESULT 1
ID Q9YRT8 PRELIMINARY: PRT; 117 AA.
AC Q9YRT8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9605NG31;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storch C., Schable C.A., Wise H., Tetch C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O.";
RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF096327; AAD04402.1; -
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT TER 117
SQ SEQUENCE 117 AA; 14156 MW; F3C6C7324386A240 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. NO. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNT 7
DB 109 LMNMFNT 115

RESULT 2

```
09YRT3
ID 09YRT3 PRELIMINARY; PRT; 117 AA.
AC 09YRT3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9605SM11;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096332; AAD04407.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14088 MW; 32ADA489B31BAFF4 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
Db 109 LMNMFNI 115

RESULT 3
09YRS7 PRELIMINARY; PRT; 117 AA.
ID 09YRS7;
AC 09YRS7;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9605SM07;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096339; AAD04414.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 14133 MW; ECBABE6A1CDA17D CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
Db 109 LMNMFNI 115
```

```
RESULT 4
09YR6 PRELIMINARY; PRT; 117 AA.
ID 09YR6;
AC 09YR6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9605SM48;
RA Sullivan P.J., Do A., Ellenberger D.L., Pau C.-P., Paul S., Kalish M.,
RA Robbins K., Lal R., Storck C., Schable C.A., Wise H., Tetteh C.,
RA Jones J., Ward J.;
RT "Surveillance of Central African Nationals living in the United States
RT reveals multiple subtypes of HIV-1 Group M and Group O."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF096350; AAD04425.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13986 MW; 39B9C97DA14BF47E CRC64;

Query Match 100.0%; Score 48; DB 15; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNMFNI 7
Db 109 LMNMFNI 115

RESULT 5
09ES6 PRELIMINARY; PRT; 118 AA.
ID 09ES6;
AC 09ES6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM103;
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plentzsek D.,
RA Lal R.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CAM103;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemu J.G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plentzsek D.,
RA Lal R.B.;
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252095; AAG14304.1;
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1
FT NON_TER 1
```

FT NON_TER 118 118
SQ SEQUENCE 118 AA; 14257 MW; C11CF6BDEFBC50 CRC64;
Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNMWNI 7
DB 105 LNMWNI 111

RESULT 6
Q9ESR9 PRELIMINARY; PRT; 118 AA.
AC Q9ESR9; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM16;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.,
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RT AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM16;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemni G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plentazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252103; AAG14311.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14159 MW; 54739ADD14A51F7 CRC64;
Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNMWNI 7
DB 105 LNMWNI 111

RESULT 7
Q9ESR8 PRELIMINARY; PRT; 118 AA.
AC Q9ESR8; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM16;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.,
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RT AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM203;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemni G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plentazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252113; AAG14322.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14173 MW; 488033169BCD3CB6 CRC64;
Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNMWNI 7
DB 105 LNMWNI 111

RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.,
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RT AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM161;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemni G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plentazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252103; AAG14312.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14244 MW; CBB698BE4A3748C3 CRC64;
Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNMWNI 7
DB 105 LNMWNI 111

RESULT 8
Q9ES08 PRELIMINARY; PRT; 118 AA.
AC Q9ES08; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM203;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.,
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RT AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM203;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemni G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plentazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252113; AAG14322.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 14173 MW; 488033169BCD3CB6 CRC64;
Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNMWNI 7
DB 105 LNMWNI 111

```
RESULT 9
Q9E5Q2 PRELIMINARY; PRT; 118 AA.
AC Q9E5Q2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM232;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM232;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnaji G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plenzazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252119; AAG14328.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41.1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 14295 MW; 807EDE44F29796AC CRC64;

Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
Db 105 LMNMFNI 111

RESULT 10
Q9E5P9 PRELIMINARY; PRT; 118 AA.
AC Q9E5P9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM256;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM256;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnaji G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plenzazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252127; AAG14336.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41.1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 14274 MW; 8B0ABECF5124B584 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
Db 105 LMNMFNI 111

RESULT 12
Q9E5P3 PRELIMINARY; PRT; 118 AA.
AC Q9E5P3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
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RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252122; AAG14331.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41.1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 14272 MW; 2C1E108925F4283C CRC64;

Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
Db 105 LMNMFNI 111

RESULT 11
Q9E5P4 PRELIMINARY; PRT; 118 AA.
AC Q9E5P4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM63;
RX MEDLINE=20414627; PubMed=10957729;
RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CAM63;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnaji G.A., Eno L.T.,
RA Ngenasong J.N., Gao F., Rayfield M., Folks T.M., Plenzazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF252127; AAG14336.1;
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41.1.
KW Transmembrane.
FT NON_TER 1 118
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 14274 MW; 8B0ABECF5124B584 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
Db 105 LMNMFNI 111

RESULT 12
Q9E5P3 PRELIMINARY; PRT; 118 AA.
AC Q9E5P3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
```


OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CAW70;
 RX MEDLINE=20414627; PubMed=10957729;
 RA Peter F.N., Eitel M.N., Judith T.N., George A.A., Laura E.T.,
 John N.N., Peng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
 RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
 Variants in Cameroon."
 RL AIDS Res. Hum. Retroviruses 16:1319-1324(2000).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=CAW70;
 RA Fongjung P.N., Mpoudi E.N., Torimiro J.N., Alemni G.A., Eno L.T.,
 Ngegasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
 RA Lal R.B.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF252128; AAC14337.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 KW Transmembrane.
 FT NON_TER 1 118
 FT NON_TER 1 118
 SQ SEQUENCE 118 AA; 14346 MW; CE454BE980AEFB1B CRC64;

Query Match 100.0%; Score 48; DB 15; Length 118;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWNI 7
 DB 105 LNMWNI 111

RESULT 13

ID 08UOX7 PRELIMINARY; PRT; 121 AA.
 AC 08UOX7;
 DT 01-MAR-2002 (TREMblrel. 20, Created)
 DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=982M072M;
 RX MEDLINE=21602569; PubMed=11739704;
 RA Traak S.A., Derdeyn C.A., Fiddell U., Chen Y., Meleth S., Kasolo F.,
 Musonda R., Hunter E., Gao F., Allen S., Hahn B.H.;
 RT "Molecular epidemiology of human immunodeficiency virus type 1
 transmission in a heterosexual cohort of discordant couples in
 Zambia."
 RL J. Virol. 76:397-405(2002).
 DR EMBL: AF405173; AAL66691.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 FT NON_TER 1 121
 FT NON_TER 1 121
 SQ SEQUENCE 121 AA; 14684 MW; F3AC3DB2FBE8802 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWNI 7
 DB 105 LNMWNI 111

RESULT 14

ID 09YXR6 PRELIMINARY; PRT; 122 AA.
 AC 09YXR6;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Envelope glycoprotein immunodominant region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RJ96BRP004;
 RA Tauri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
 Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
 RA Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."
 RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF034037; AAC79289.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 KW Transmembrane.
 FT NON_TER 1 122
 FT NON_TER 1 122
 SQ SEQUENCE 122 AA; 14702 MW; 873C9A28AE14BA78 CRC64;

Query Match 100.0%; Score 48; DB 15; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWNI 7
 DB 109 LNMWNI 115

RESULT 15

ID 09YXP1 PRELIMINARY; PRT; 122 AA.
 AC 09YXP1;
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Envelope glycoprotein immunodominant region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RJ96BRP081;
 RA Tauri A., Swanson P.A., Devare S.G., Berro O.J., Savedra A.,
 Costa L.J., Telles J.G., Brindeiro R., Schable C., Pieniazek D.,
 RA Rayfield M.;
 RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil."
 RL Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF034062; AAC79314.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR Pfam: PF00517; Gp41; 1.
 KW Transmembrane.
 FT NON_TER 1 122
 FT NON_TER 1 122
 SQ SEQUENCE 122 AA; 14778 MW; FD3191CE79ABBI9D CRC64;

Query Match 100.0%; Score 48; DB 15; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWNI 7
 DB 109 LNMWNI 115

Wed May 7 14:34:38 2003

us-09-877-606-7.rspt

Page 6

Search completed: May 7, 2003, 09:57:21
Job time : 6.02315 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 2.07407 Seconds
(without alignments)
99.302 Million cell updates/sec

Title: US-09-877-606-7
Perfect score: 48
Sequence: 1 LMWNT 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfilest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	20	1 US-08-218-025A-7	Sequence 7, Appli
2	48	100.0	23	1 US-08-218-025A-152	Sequence 152, App
3	48	100.0	36	3 US-08-484-223B-232	Sequence 232, App
4	48	100.0	36	3 US-08-484-223B-233	Sequence 233, App
5	48	100.0	36	4 US-09-082-279B-549	Sequence 549, App
6	48	100.0	36	4 US-09-082-279B-550	Sequence 550, App
7	48	100.0	36	4 US-09-082-279B-551	Sequence 551, App
8	48	100.0	36	4 US-09-082-279B-552	Sequence 552, App
9	48	100.0	36	4 US-09-082-279B-553	Sequence 553, App
10	48	100.0	36	4 US-09-082-279B-554	Sequence 554, App
11	48	100.0	36	4 US-09-082-279B-555	Sequence 555, App
12	48	100.0	36	4 US-09-082-279B-556	Sequence 556, App
13	48	100.0	36	4 US-09-082-279B-557	Sequence 557, App
14	48	100.0	36	4 US-09-082-279B-558	Sequence 558, App
15	48	100.0	36	4 US-09-082-279B-559	Sequence 559, App
16	48	100.0	36	4 US-09-082-279B-560	Sequence 560, App
17	48	100.0	36	4 US-08-474-349A-401	Sequence 401, App
18	48	100.0	36	4 US-08-474-349A-402	Sequence 402, App
19	48	100.0	36	4 US-08-474-349A-403	Sequence 403, App
20	48	100.0	36	4 US-08-474-349A-404	Sequence 404, App
21	48	100.0	36	4 US-08-474-349A-405	Sequence 405, App
22	48	100.0	36	4 US-08-474-349A-406	Sequence 406, App
23	48	100.0	36	4 US-08-474-349A-407	Sequence 407, App
24	48	100.0	36	4 US-08-474-349A-408	Sequence 408, App
25	48	100.0	36	4 US-08-474-349A-409	Sequence 409, App
26	48	100.0	36	4 US-08-474-349A-410	Sequence 410, App
27	48	100.0	36	4 US-08-474-349A-411	Sequence 411, App

28	48	100.0	36	4 US-08-474-349A-412	Sequence 412, App
29	48	100.0	36	4 US-09-315-304B-549	Sequence 549, App
30	48	100.0	36	4 US-09-315-304B-550	Sequence 550, App
31	48	100.0	36	4 US-09-315-304B-551	Sequence 551, App
32	48	100.0	36	4 US-09-315-304B-552	Sequence 552, App
33	48	100.0	36	4 US-09-315-304B-553	Sequence 553, App
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35	48	100.0	36	4 US-09-315-304B-555	Sequence 555, App
36	48	100.0	36	4 US-09-315-304B-556	Sequence 556, App
37	48	100.0	36	4 US-09-315-304B-557	Sequence 557, App
38	48	100.0	36	4 US-09-315-304B-558	Sequence 558, App
39	48	100.0	36	4 US-09-315-304B-559	Sequence 559, App
40	48	100.0	36	4 US-09-315-304B-560	Sequence 560, App
41	48	100.0	38	4 US-09-082-279B-776	Sequence 776, App
42	48	100.0	38	4 US-09-315-304B-776	Sequence 776, App
43	48	100.0	39	4 US-09-082-279B-777	Sequence 777, App
44	48	100.0	39	4 US-09-315-304B-777	Sequence 777, App
45	48	100.0	40	4 US-09-082-279B-778	Sequence 778, App

ALIGNMENTS

RESULT 1
US-08-218-025A-7
Sequence 7, Application US/08218025A
Patent No. 5556774

GENERAL INFORMATION:

APPLICANT: Weiner, David B.
APPLICANT: Ugen, Kenneth E.
APPLICANT: Williams, William V.
TITLE OF INVENTION: Methods and Compositions for Diagnosing
TITLE OF INVENTION: and Treating Certain HIV Infected Patients
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:

ADDRESS: Howson and Howson
STREET: P.O. Box 457, 321 No. 555674Aristown Road
CITY: Spring House
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/218,025A
FILING DATE: 24-MAR-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/891,451
FILING DATE: 29-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST33A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 540-9206

TELEFAX: (215) 540-5618

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

Query Match 100.0%; Score 48; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LMWNT 7

Db 8 LMNMENI 14

RESULT 2

US-08-218-025A-152
Sequence 152, Application US/08218025A

Patent No. 5556744

GENERAL INFORMATION:

APPLICANT: Weiner, David B.

APPLICANT: Ugen, Kenneth E.

APPLICANT: Williams, William V.

TITLE OF INVENTION: Methods and Compositions for Diagnosing

TITLE OF INVENTION: and Treating Certain HIV Infected Patients

NUMBER OF SEQUENCES: 197

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: P.O. Box 457, 321 No. 55567441sttown Road

CITY: Spring House

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/218,025A

FILING DATE: 24-MAR-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/891,451

FILING DATE: 29-MAY-1992

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: W5133A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 540-9206

TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 152:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-218-025A-152

Query Match

Best Local Similarity: 100.0%; Score 48; DB 1; Length 23;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMENI 7

Db 9 LMNMENI 15

RESULT 3

US-08-484-223B-232

Sequence 232, Application US/08484223B

Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Biologuesl, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Peteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 232:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-484-223B-232

Query Match

Best Local Similarity: 100.0%; Score 48; DB 3; Length 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMENI 7

Db 30 LMNMENI 36

RESULT 4

US-08-484-223B-233

Sequence 233, Application US/08484223B

Patent No. 6020459

GENERAL INFORMATION:

APPLICANT: Biologuesl, Dani P.

APPLICANT: Matthews, Thomas J.

APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.

APPLICANT: Peteway, Stephen R.

APPLICANT: Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

TITLE OF INVENTION: TRANSMISSION

NUMBER OF SEQUENCES: 245

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 233:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-223B-233

Query Match 100.0%; Score 48; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
DB 29 LMNMFNI 35

RESULT 5
US-09-082-279B-549
Sequence 549, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 549
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-549

Query Match 100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
DB 19 LMNMFNI 25

RESULT 6
US-09-082-279B-550
Sequence 550, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 550
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-550

Query Match 100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
DB 20 LMNMFNI 26

RESULT 7
US-09-082-279B-551
Sequence 551, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 551
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-082-279B-551

Query Match 100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
DB 21 LMNMFNI 27

RESULT 8
US-09-082-279B-552
Sequence 552, Application US/09082279B
Patent No. 6258782
GENERAL INFORMATION:
APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Anwer, Mohamed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515

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;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 552
;; LENGTH: 36
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;;   OTHER INFORMATION: Core polypeptide
US-09-082-279B-552

Query Match          100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFNI 7
    |||||
Db 22 LMNWFNI 28

RESULT 9
US-09-082-279B-553
; Sequence 553, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
;   APPLICANT: Barney, Shawn
;   APPLICANT: Guthrie, Kelly
;   APPLICANT: Merutka, Gene
;   APPLICANT: Anwer, Mohamed
;   TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
;   FILE REFERENCE: 7872-043
;   CURRENT APPLICATION NUMBER: US/09/082,279B
;   CURRENT FILING DATE: 1998-05-20
;   NUMBER OF SEQ ID NOS: 1515
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 553
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Core polypeptide
US-09-082-279B-553

Query Match          100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFNI 7
    |||||
Db 23 LMNWFNI 29

RESULT 10
US-09-082-279B-554
; Sequence 554, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
;   APPLICANT: Barney, Shawn
;   APPLICANT: Guthrie, Kelly
;   APPLICANT: Merutka, Gene
;   APPLICANT: Anwer, Mohamed
;   TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
;   FILE REFERENCE: 7872-043
;   CURRENT APPLICATION NUMBER: US/09/082,279B
;   CURRENT FILING DATE: 1998-05-20
;   NUMBER OF SEQ ID NOS: 1515
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 554
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;; FEATURE:
;;   OTHER INFORMATION: Core polypeptide
US-09-082-279B-554

Query Match          100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFNI 7
    |||||
Db 24 LMNWFNI 30

RESULT 11
US-09-082-279B-555
; Sequence 555, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
;   APPLICANT: Barney, Shawn
;   APPLICANT: Guthrie, Kelly
;   APPLICANT: Merutka, Gene
;   APPLICANT: Anwer, Mohamed
;   TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
;   FILE REFERENCE: 7872-043
;   CURRENT APPLICATION NUMBER: US/09/082,279B
;   CURRENT FILING DATE: 1998-05-20
;   NUMBER OF SEQ ID NOS: 1515
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 555
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Core polypeptide
US-09-082-279B-555

Query Match          100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFNI 7
    |||||
Db 25 LMNWFNI 31

RESULT 12
US-09-082-279B-556
; Sequence 556, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
;   APPLICANT: Barney, Shawn
;   APPLICANT: Guthrie, Kelly
;   APPLICANT: Merutka, Gene
;   APPLICANT: Anwer, Mohamed
;   TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
;   FILE REFERENCE: 7872-043
;   CURRENT APPLICATION NUMBER: US/09/082,279B
;   CURRENT FILING DATE: 1998-05-20
;   NUMBER OF SEQ ID NOS: 1515
;   SOFTWARE: FastSeq for Windows Version 3.0
;   SEQ ID NO 556
;   LENGTH: 36
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Core polypeptide
US-09-082-279B-556

Query Match          100.0%; Score 48; DB 4; Length 36;
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Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMENI 7
|||||||
Db 26 LMNMENI 32

RESULT 13
US-09-082-279B-557
; Sequence 557, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 557
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-557

Query Match 100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMENI 7
|||||||
Db 27 LMNMENI 33

RESULT 14
US-09-082-279B-558
; Sequence 558, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 558
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-558

Query Match 100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMENI 7
|||||||

Db 28 LMNMENI 34

RESULT 15
US-09-082-279B-559
; Sequence 559, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 559
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-559

Query Match 100.0%; Score 48; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMENI 7
|||||||
Db 29 LMNMENI 35

Search completed: May 7, 2003, 09:59:51
Job time : 2.07407 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 3.85648 Seconds
(without alignments)
167.038 Million cell updates/sec

Title: US-09-877-606-7
Perfect score: 48
Sequence: 1 LMNMFNI 7

Scoring table: BLOSUM62
Gapco 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues
Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_A1.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	56	10	US-09-779-451-4
2	48	100.0	177	9	US-10-040-349B-2
3	48	100.0	221	9	US-10-059-271-84
4	48	100.0	232	9	US-10-059-271-81
5	48	100.0	254	9	US-10-059-271-82
6	48	100.0	256	9	US-10-059-271-97
7	48	100.0	268	10	US-09-854-816-9
8	48	100.0	268	10	US-09-854-816-10
9	48	100.0	268	10	US-09-854-816-16
10	48	100.0	268	10	US-09-854-816-17
11	48	100.0	268	10	US-09-854-816-18
12	48	100.0	268	10	US-09-854-816-19
13	48	100.0	268	10	US-09-854-816-41
14	48	100.0	269	10	US-09-854-816-12
15	48	100.0	269	10	US-09-854-816-31
16	48	100.0	269	10	US-09-854-816-43
17	48	100.0	269	10	US-09-854-816-44
18	48	100.0	269	10	US-09-854-816-46
19	48	100.0	344	9	US-10-040-349B-1

20	48	100.0	345	9	US-10-026-741-49	Sequence 49, Appl
21	48	100.0	345	10	US-09-779-451-8	Sequence 8, Appl
22	48	100.0	391	9	US-10-059-271-93	Sequence 93, Appl
23	48	100.0	519	10	US-09-756-551A-8	Sequence 8, Appl
24	48	100.0	844	10	US-09-991-258-19	Sequence 19, Appl
25	48	100.0	853	9	US-10-003-035-33	Sequence 33, Appl
26	48	100.0	856	10	US-09-476-242-1	Sequence 1, Appl
27	48	100.0	861	9	US-10-026-741-103	Sequence 103, Appl
28	48	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl
29	48	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl
30	44	91.7	37	10	US-09-779-451-68	Sequence 68, Appl
31	44	91.7	47	10	US-09-779-451-66	Sequence 66, Appl
32	43	89.6	145	12	US-10-000-321-11	Sequence 11, Appl
33	43	89.6	146	12	US-10-000-321-10	Sequence 10, Appl
34	43	89.6	233	10	US-09-854-816-50	Sequence 50, Appl
35	43	89.6	233	43	US-09-854-816-51	Sequence 51, Appl
36	43	89.6	267	10	US-09-854-816-15	Sequence 15, Appl
37	43	89.6	268	10	US-09-854-816-8	Sequence 8, Appl
38	43	89.6	268	10	US-09-854-816-13	Sequence 13, Appl
39	43	89.6	268	10	US-09-854-816-14	Sequence 14, Appl
40	43	89.6	268	10	US-09-854-816-26	Sequence 26, Appl
41	43	89.6	268	10	US-09-854-816-35	Sequence 35, Appl
42	43	89.6	268	10	US-09-854-816-39	Sequence 39, Appl
43	43	89.6	268	10	US-09-854-816-68	Sequence 68, Appl
44	43	89.6	268	10	US-09-854-816-70	Sequence 70, Appl
45	43	89.6	268	10	US-09-854-816-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1
US-09-779-451-4
Sequence 4, Application US/09779451
Patent No. US20020094521A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
APPLICANT: Allway, Graham P.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4

Query Match 100.0%; Score 48; DB 10; Length 56;
Best local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNMFNI 7
Db 47 LMNMFNI 53

RESULT 2
US-10-040-349B-2
Sequence 2, Application US/10040349B
GENERAL INFORMATION:
APPLICANT: Brasseaux, Robert
APPLICANT: Charlotiaux, Benoit
APPLICANT: Chevallier, Michel
APPLICANT: El Habib, Raphaelle
APPLICANT: Krell, Tino

;; TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
;; FILE REFERENCE: 01-078-A
;; CURRENT APPLICATION NUMBER: US/10/040,349B
;; CURRENT FILING DATE: 2002-07-09
;; NUMBER OF SEQ ID NOS: 2
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 177
;; TYPE: PPT
;; ORGANISM: Human Immunodeficiency Virus type 1
;; FEATURE:
;; NAME/KEY: Peptide
;; LOCATION: (1)..(177)
;; OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2

Query Match 100.0%; Score 48; DB 9; Length 177;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
|||||
DB 135 LMNWFNI 141

RESULT 3
US-10-059-271-84
;; Sequence 84, Application US/10059271
;; Publication No. US20030082208A1
;; GENERAL INFORMATION:
;; APPLICANT: REPE, HEINRICH
;; APPLICANT: BUDE, ECKHARD
;; APPLICANT: NICOLAUS, STEFAN
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
;; FILE REFERENCE: ABBRE-22
;; CURRENT APPLICATION NUMBER: US/10/059,271
;; CURRENT FILING DATE: 2002-01-31
;; PRIOR APPLICATION NUMBER: DE 101 06 295
;; PRIOR FILING DATE: 2001-02-02
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 84
;; LENGTH: 221
;; TYPE: PPT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84

Query Match 100.0%; Score 48; DB 9; Length 221;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
|||||
DB 162 LMNWFNI 168

RESULT 4
US-10-059-271-81
;; Sequence 81, Application US/10059271
;; Publication No. US20030082208A1
;; GENERAL INFORMATION:
;; APPLICANT: REPE, HEINRICH
;; APPLICANT: BUDE, ECKHARD
;; APPLICANT: NICOLAUS, STEFAN
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
;; FILE REFERENCE: ABBRE-22
;; CURRENT APPLICATION NUMBER: US/10/059,271
;; CURRENT FILING DATE: 2002-01-31

;; PRIOR APPLICATION NUMBER: DE 101 06 295
;; PRIOR FILING DATE: 2001-02-02
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 81
;; LENGTH: 232
;; TYPE: PPT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-81

Query Match 100.0%; Score 48; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
|||||
DB 175 LMNWFNI 181

RESULT 5
US-10-059-271-82
;; Sequence 82, Application US/10059271
;; Publication No. US20030082208A1
;; GENERAL INFORMATION:
;; APPLICANT: REPE, HEINRICH
;; APPLICANT: BUDE, ECKHARD
;; APPLICANT: NICOLAUS, STEFAN
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
;; FILE REFERENCE: ABBRE-22
;; CURRENT APPLICATION NUMBER: US/10/059,271
;; CURRENT FILING DATE: 2002-01-31
;; PRIOR APPLICATION NUMBER: DE 101 06 295
;; PRIOR FILING DATE: 2001-02-02
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 82
;; LENGTH: 254
;; TYPE: PPT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-82

Query Match 100.0%; Score 48; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMNWFNI 7
|||||
DB 197 LMNWFNI 203

RESULT 6
US-10-059-271-97
;; Sequence 97, Application US/10059271
;; Publication No. US20030082208A1
;; GENERAL INFORMATION:
;; APPLICANT: REPE, HEINRICH
;; APPLICANT: BUDE, ECKHARD
;; APPLICANT: NICOLAUS, STEFAN
;; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
;; FILE REFERENCE: ABBRE-22
;; CURRENT APPLICATION NUMBER: US/10/059,271
;; CURRENT FILING DATE: 2002-01-31
;; PRIOR APPLICATION NUMBER: DE 101 06 295
;; PRIOR FILING DATE: 2001-02-02
;; NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 97
LENGTH: 256
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Peptide
US-10-059-271-97

Query Match 100.0%; Score 48; DB 9; Length 256;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWNT 7
|||||
Db 197 LNMWNT 203

RESULT 7
US-09-854-816-9
Sequence 9, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-854-816-9

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWNT 7
|||||

Db 199 LNMWNT 205

RESULT 8
US-09-854-816-10
Sequence 10, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/854,816

FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-854-816-10

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWNT 7
|||||
Db 199 LNMWNT 205

RESULT 9
US-09-854-816-16
Sequence 16, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted

J. Kevin Judice

Robert S. McDowell

J. Christopher Phelan

Melissa A. Starovasnik

James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-854-816-16
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMWPMI 7
Db 199 LMWPMI 205
RESULT 10
US-09-854-816-17
Sequence 17, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted,
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-854-816-17
Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMWPMI 7
Db 199 LMWPMI 205
RESULT 11
US-09-854-816-18
Sequence 18, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted,
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-854-816-18

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFI 7
1111111
DB 199 LNMWFI 205

RESULT 12
US-09-854-816-19
Sequence 19, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasilk
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-854-816-19

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFI 7
1111111
DB 199 LNMWFI 205

RESULT 13
US-09-854-816-41
Sequence 41, Application US/09854816
Patent No. US20020151473A1

GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasilk
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Phd., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-854-816-41

Query Match 100.0%; Score 48; DB 10; Length 268;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWFI 7
1111111
DB 199 LNMWFI 205

RESULT 14
US-09-854-816-12
Sequence 12, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasilk
James A. Wells

TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same

NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

```

: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/854,816
: FILING DATE: 15-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/965,056
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, PhD., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P1005R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 269 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 12:
: US-09-854-816-12

Query Match      100.0%; Score 48; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFNI 7
Db 200 LMNWFNI 206

RESULT 15
US-09-854-816-31
: Sequence 31, Application US/09854816
: Patent No. US20020151473A1
: GENERAL INFORMATION:
: APPLICANT: Andrew C. Braisted
: J. Kevin Judice
: Robert S. McDowell
: J. Christopher Phelan
: Melissa A. Starovasnik
: James A. Wells
: TITLE OF INVENTION: Constrained Helical Peptides and Methods of
: Making Same
: NUMBER OF SEQUENCES: 113
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/854,816
: FILING DATE: 15-May-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/965,056
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Torchia, PhD., Timothy E.
: REGISTRATION NUMBER: 36,700
: REFERENCE/DOCKET NUMBER: P1005R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 269 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 12:
: US-09-854-816-12

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: REFERENCE/DOCKET NUMBER: P1005R2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-8674
: TELEFAX: 650/952-9881
: INFORMATION FOR SEQ ID NO: 31:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 269 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 31:
: US-09-854-816-31

Query Match      100.0%; Score 48; DB 10; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMNWFNI 7
Db 200 LMNWFNI 206

Search completed: May 7, 2003, 10:21:55
Job time : 3.85648 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:40:21 ; Search time 6.38426 Seconds

(without alignments)
146,102 Million cell updates/sec

Title: US-09-877-606-8

Perfect score: 7
Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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22: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT.*
23: /SID2/gcgdata/geneseq/genesep-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the peptide being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	1	20	AA46552
2	0	0.0	1	22	AB856870
3	0	0.0	1	22	AB866809
4	0	0.0	1	22	AB866810
5	0	0.0	1	22	AB862941
6	0	0.0	1	22	AA97643
7	0	0.0	1	22	AA97834
8	0	0.0	1	22	AA97974
9	0	0.0	1	22	AA98354
10	0	0.0	1	22	AA98447

11	0	0.0	1	22	AA53218	Human nonconservat
12	0	0.0	1	22	AA53219	Human nonconservat
13	0	0.0	1	22	AA53290	Human nonconservat
14	0	0.0	1	22	AA53291	Human nonconservat
15	0	0.0	1	22	AA53328	Human nonconservat
16	0	0.0	1	22	AA53329	Human nonconservat
17	0	0.0	1	22	AA45230	Human nonconservat
18	0	0.0	1	22	AA69966	Hill binding site C
19	0	0.0	1	22	AA69983	ERA binding domain
20	0	0.0	1	22	AA69987	ERA binding domain
21	0	0.0	1	22	AA69988	ERA binding domain
22	0	0.0	1	22	AA69989	ERA binding domain
23	0	0.0	1	22	AA69990	ERA binding domain
24	0	0.0	1	22	AA69991	ERA binding domain
25	0	0.0	1	22	AA69992	ERA binding domain
26	0	0.0	1	22	AA69993	ERA binding domain
27	0	0.0	1	22	AA69994	ERA binding domain
28	0	0.0	1	22	AA69995	ERA binding domain
29	0	0.0	1	22	AA69996	ERA binding domain
30	0	0.0	1	22	AA69997	ERA binding domain
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45	0	0.0	1	22	AA69999	ERA binding domain

ALIGNMENTS

RESULT 1	AA46552	
ID	AA46552	standard; Peptide: 1 AA.
XX	AA46552;	
AC	AA46552;	
XX	AA46552;	
DT	01-DEC-1999	(first entry)
XX	01-DEC-1999	
DE	Immunogenic peptide having a human leukocyte antigen binding motif #1263.	
XX	Immunogenic antigen; binding: immunogenic; glycoprotein; MHC; HLA;	
XX	immune response; T cell activation; major histocompatibility complex;	
KW	cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;	
KW	prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;	
KW	vaccine; immunisation.	
OS	Synthetic.	
XX	Homo sapiens.	
PN	WO9945954-A1.	
PD	16-SEP-1999.	
XX	16-SEP-1999.	
PF	13-MAR-1998;	98WO-US05039.
XX	13-MAR-1998;	
PR	13-MAR-1998;	98WO-US05039.
XX	13-MAR-1998;	
PA	(EPIM-) EPIMONE INC.	
XX	Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;	
PI	WPI: 1999-551214/46.	
XX	WPI: 1999-551214/46.	

PT New immunogenic peptides with HLA binding motif, useful in treatment
PT and diagnosis of cancers and viral diseases -
PS Claim 1; Page 80; 150pp; English.
XX
XX
CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
SQ Sequence 1 AA;
XX
XX
Query Match 0.0%; Score 0; DB 20; Length 1;
Best Local Similarity 0.0%; Pred No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 x 1
DB 1 x 1
RESULT 2
ABB56870
ID ABB56870 standard; Peptide; 1 AA.
XX
XX ABB56870;
AC
XX
DT 05-MAR-2002 (first entry)
XX
XX Human SNP related amino acid sequence SEQ ID NO:1435.
DE
XX
XX Human: single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neutroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein.
XX
XX Homo sapiens.
OS
XX WO200138586-A2.
PN
XX
XX 31-MAY-2001.
PD
XX
XX 22-NOV-2000; 2000WO-US32311.
PF
XX
XX 24-NOV-1999; 99US-0167383.
PR
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX Shimkets RA, Leach M;
PI
XX
XX WPI: 2001-355949/37.
DR
XX
XX Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a
PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
PT sequence polymorphism -

XX
XX Claim 1; Page 666; 674pp; English.
PS
XX
XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neutroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the
CC polymorphic protein within appropriate physiological samples).
SQ Sequence 1 AA;
XX
XX
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 x 1
DB 1 s 1
RESULT 3
ABB66809
ID ABB66809 standard; Protein; 1 AA.
XX
XX ABB66809;
AC
XX
DT 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 27219.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical.
KW
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
PA
XX
XX (PEKE) PE CORP NY.
PI
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX
XX WPI: 2001-656860/75.
DR
XX
XX N-PSDB; ABL10912.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT
XX
XX Disclosure: SEQ ID NO 27219; 21pp + Sequence listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABLL16-ABLJ30511), expressed DNA
CC sequences (ABLL1840-ABLL16175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 1 AA;

Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 H 1

RESULT 4
ABBS6810
ID ABB66810 standard; Protein; 1 AA.

AC ABB66810;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 27222.

XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PMD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB: ABL10913.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -

PS Disclosure: SEQ ID NO 27222; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABLL16176-ABLL30511), expressed DNA
CC sequences (ABLL1840-ABLL16175) and the encoded proteins
CC (ABBS7737-ABBS72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 1 AA;

Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 H 1

RESULT 5
ABG02941
ID ABG02941 standard; Protein; 1 AA.

XX ABB02941;

XX 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #2932.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YF;

XX WPI: 2001-639362/73.

DR N-PSDB: AAS67128.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 20; SEQ ID NO 33300; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 1 AA;

Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

Db 1 M 1

RESULT 6

ID AAM97643 standard; Peptide: 1 AA.

AC AAM97643;

DT 24-JAN-2002 (first entry)

DE Human peptide #918 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PR oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -

PS Disclosure: Page 3869; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.

SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 22; Length 1;

Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 x 1

Db 1 C 1

RESULT 7

ID AAM97834 standard; Peptide: 1 AA.

AC AAM97834;

DT 24-JAN-2002 (first entry)

DE Human peptide #1109 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2001-465210/50.

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PR oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -

PS Disclosure: Page 3911; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.

SQ Sequence 1 AA;

Query Match 0.0%; Score 0; DB 22; Length 1;

Best Local Similarity 0.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 x 1

Db 1 E 1

RESULT 8

ID AAM97974 standard; Peptide: 1 AA.

XX
AC AAM97974;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1249 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX
PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX
PT cancer, autoimmune diseases and infections -
XX
PS Disclosure; Page 3941; 4143pp; English.
XX
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. Rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX
SQ Sequence 1 AA;
XX
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 X 1
DB 1 L 1
RESULT 9
AAM98354 standard; Peptide; 1 AA.
ID AAM98354
XX
AC AAM98354;
XX

DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1629 encoded by a SNP oligonucleotide.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US35498.
XX
PR 28-DEC-1999; 99US-0173419.
XX
PR 27-DEC-2000; 2000US-0173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX
PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX
PT cancer, autoimmune diseases and infections -
XX
PS Disclosure; Page 4025; 4143pp; English.
XX
XX
CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. Rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX
SQ Sequence 1 AA;
XX
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 X 1
DB 1 S 1
RESULT 10
AAM98447 standard; Peptide; 1 AA.
ID AAM98447
XX
AC AAM98447;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #1722 encoded by a SNP oligonucleotide.

XX immunosuppressive; immunostimulatory; antinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
OS Homo sapiens.
XX WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000WO-US35498.
XX PR 28-DEC-1999; 99US-0173419.
XX PR 27-DEC-2000; 2000US-0173419.
XX (CURA-) CURAGEN CORP.
XX PA Shinkets RA, Leach M;
XX PI WPI: 2001-465210/50.
XX DR polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosis and treating, e.g.
XX PT cancer, autoimmune diseases and infections -
XX PS Disclosure: Page 4045; 4143pp; English.
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms.
XX SQ Sequence 1 AA:
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 X 1
DB 1 L 1
RESULT 11
AAM53218
ID AAM53218 standard; Peptide: 1 AA.
XX AAM53218;
AC AAM53218;
XX 09-NOV-2001 (first entry)
DT Human nonconservative amino acid changing SNP related peptide SEQ.6913.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
XX

KW quantitation; restorative therapy; polymorphic.
XX OS Homo sapiens.
XX WO200140521-A2.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US32758.
XX PR 30-NOV-1999; 99US-0168138.
XX PR 29-NOV-2000; 2000US-0726173.
XX (CURA-) CURAGEN CORP.
XX PA Shinkets RA, Leach M;
XX PI WPI: 2001-356160/37.
XX DR polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy -
XX PS Claim 29; Page 2619; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA173114 to AA173329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the peptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX SQ Sequence 1 AA:
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 X 1
DB 1 H 1
RESULT 12
AAM53219
ID AAM53219 standard; Peptide: 1 AA.
XX AAM53219;
AC AAM53219;
XX 09-NOV-2001 (first entry)
DT Human nonconservative amino acid changing SNP related peptide SEQ.6914.
DE Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic.
XX OS Homo sapiens.
XX WO200140521-A2.
XX

PD 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Shinkets RA, Leach M;
XX
XX WPI: 2001-356160/37.
DR
XX polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
XX Claim 29; Page 2619; 2653pp; English.
PS
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
CC
XX
SQ Sequence 1 AA;
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 x 1
Db 1 H 1
RESULT 13
AAM53290
ID AAM53290 standard; Peptide; 1 AA.
XX
XX AAM53290;
AC
XX 09-NOV-2001 (first entry)
DT
XX
XX Human nonconservative amino acid changing SNP related peptide SEQ:6985.
DE
XX
XX Human: single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US32758.
PF
XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
PR

XX
XX (CURA-) CURAGEN CORP.
PA
XX Shinkets RA, Leach M;
XX
XX WPI: 2001-356160/37.
DR
XX
XX polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
XX Claim 29; Page 2641; 2653pp; English.
PS
XX AAT73060 to AAT79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
CC
XX
SQ Sequence 1 AA;
Query Match 0.0%; Score 0; DB 22; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 x 1
Db 1 L 1
RESULT 14
AAM53291
ID AAM53291 standard; Peptide; 1 AA.
XX
XX AAM53291;
AC
XX 09-NOV-2001 (first entry)
DT
XX
XX Human nonconservative amino acid changing SNP related peptide SEQ:6986.
DE
XX
XX Human: single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic.
XX
XX Homo sapiens.
OS
XX
XX WO200140521-A2.
PN
XX
XX 07-JUN-2001.
PD
XX 30-NOV-2000; 2000WO-US32758.
PF
XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
PR
XX (CURA-) CURAGEN CORP.
PA
XX Shinkets RA, Leach M;
XX
XX WPI: 2001-356160/37.
DR

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 2.36574 Seconds

(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-8

Perfect score: 7

Sequence: 1 XXXXXX 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	3	3	thyroliberin - Bom
2	0	0.0	3	3	thyroliberin - pig
3	0	0.0	3	3	thyroliberin - she
4	0	0.0	3	3	thyroliberin - eas
5	0	0.0	3	3	growth-modulating
6	0	0.0	3	3	burstin - chicken
7	0	0.0	3	3	spinal cord peptid
8	0	0.0	3	3	thyroctroptin-releas
9	0	0.0	3	3	R-phycocerythrin al
10	0	0.0	3	3	angiotensin-conver
11	0	0.0	3	3	hustidinol dehydro
12	0	0.0	3	3	TRH-like tripeptid
13	0	0.0	3	3	bradykinin-potent
14	0	0.0	3	3	bradykinin-potent
15	0	0.0	3	3	gene p20k protein
16	0	0.0	3	3	T-cell receptor be
17	0	0.0	3	3	T-cell receptor be
18	0	0.0	3	3	T-cell receptor be
19	0	0.0	3	3	T-cell receptor be
20	0	0.0	3	3	T-cell receptor be
21	0	0.0	3	3	tyrosine protein k
22	0	0.0	3	3	blood cell protein
23	0	0.0	3	3	cytochrome-c oxida
24	0	0.0	4	1	antho-Ramide neur
25	0	0.0	4	2	thyroglobulin - do
26	0	0.0	4	2	phagocytosis-stimu
27	0	0.0	4	2	tyrosine-melanocyt
28	0	0.0	4	2	cardioexcitatory n
29	0	0.0	4	2	carbon-monoxide de

30	0	0.0	4	2	Pt0146	carbon-monoxide de
31	0	0.0	4	2	A37832	phenol 2-monooxyge
32	0	0.0	4	2	A48360	gamma subunit of p
33	0	0.0	4	2	I40697	biotin A - Citropa
34	0	0.0	4	2	A61300	22k superhelical D
35	0	0.0	4	2	I57745	D-mannanate hydrol
36	0	0.0	4	2	A41890	protein D - Escher
37	0	0.0	4	2	S43014	hypothetical prote
38	0	0.0	4	2	D41654	hypothetical prote
39	0	0.0	4	2	B43848	cell surface adhes
40	0	0.0	4	2	I40505	hypothetical prote
41	0	0.0	4	2	I40870	phospholipase C (E
42	0	0.0	4	2	I40804	endoglycanase F -
43	0	0.0	4	2	T46627	hypothetical prote
44	0	0.0	4	2	S09478	globulin IV alpha
45	0	0.0	4	2	S53508	starvation-induced

ALIGNMENTS

RESULT 1

thyroliberin - Bombina orientalis

C:Species: Bombina orientalis

C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A90919; A01415

R:Yasuhara, T.; Nakajima, T.

Chem. Pharm. Bull. 23, 3301-3303, 1975

A:Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A:Reference number: A90919; MUID:76138399; PMID:815011

A:Accession: A90919

A:Residues: 1-3 <YAS>

A:Molecule type: protein

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 Q 1

RESULT 2

thyroliberin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A01415

R:Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A:Title: Structure of porcine thyroctroptin releasing hormone.

A:Reference number: A90560; MUID:70136150; PMID:4984938

A:Accession: A01415

A:Molecule type: protein

A:Residues: 1-3 <NAI>

R:Boiler, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A:Title: The identity of chemical and hormonal properties of the thyroctroptin releasin

A:Reference number: A90167; MUID:70039904; PMID:4982117

A:Contents: annotation

A:Note: biological activities and Rf values (in 17 chromatographic systems) of the sy

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Q 1

RESULT 3

RHSRT

thyroliberin - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A93750; A01415

R:Desiderio Jr., D.M.; Burgess, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5, 221-228, 1971

A:Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating

A:Reference number: A93750

A:Accession: A93750

A:Molecule type: protein

A:Residues: 1-3 <DES>

R:Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A:Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A:Reference number: A93101; MUID:70163386; PMID:4985794

A:Contents: annotation

A>Note: physicochemical characteristics and biological activities of the natural and syn

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match

Best Local Similarity 0.0%; Score 0; DB 3; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Q 1

RESULT 4

A92971

thyroliberin - eastern newt (tentative sequence)

C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A92971; A01415

R:Griffith-Jorgensen, Y.; McKelvy, J.F.

J. Neurochem. 23, 471-478, 1974

A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) bra

A:Reference number: A92971; MUID:75035605; PMID:4214528

A:Accession: A92971

A:Molecule type: protein

A:Residues: 1-3 <GR1>

A>Note: a peptide with the chromatographic and electrophoretic characteristics of thyrol

istidine, or glutamic acid

C:Superfamily: thyroliberin precursor

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match

Best Local Similarity 0.0%; Score 0; DB 3; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Q 1

RESULT 5

GKHD

growth-modulating peptide - human

C:Species: Homo sapiens (man)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A01421

R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.

Experientia 33, 324-325, 1977

A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.

A:Reference number: A01421; MUID:77162369; PMID:858356

A:Accession: A01421

A:Molecule type: protein

A:Residues: 1-3 <SCH>

A>Note: this serum tripeptide is found to stimulate growth of some cell types and to

C:Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 0.0%; Score 0; DB 3; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 G 1

RESULT 6

A60898

bursin - chicken

C:Species: Gallus gallus (chicken)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A60898

R:Audhy, T.; Kroon, D.; Heavner, G.; Vilmones, G.; Goldstein, G.

Science 231, 997-999, 1986

A:Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone o

A:Reference number: A60898; MUID:86122916; PMID:3484838

A:Accession: A60898

A:Molecule type: protein

A:Residues: 1-3 <AUD>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; hormone

F:3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 0.0%; Score 0; DB 3; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 K 1

RESULT 7

A23751

spinal cord peptide SCP-4 - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C:Accession: A23751

R:HSI, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou

Arch. Biochem. Biophys. 240, 178-183, 1985

A:Reference number: A23751; MUID:85250425; PMID:4015098

A:Accession: A23751

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <HS1>

C:Superfamily: unassigned animal peptides

Query Match

Best Local Similarity 0.0%; Score 0; DB 3; Length 3;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 Q 1

RESULT 8

B23751
spinal cord peptide SCP-5 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: B23751
R:Hi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, K.
Arch. Biochem. Biophys. 240, 178-183, 1985
A:Reference number: A23751; MUID:85250425; PMID:4015098
A:Accession: B23751
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <HS1>
C:Superfamily: unassigned animal peptides

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 M 1

RESULT 9
A33802
thyrotropin-releasing hormone-like peptide - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A33802
R:Cockle, S.M.; Altken, A.; Beg, F.; Smyth, D.G.
J. Biol. Chem. 264, 7786-7791, 1989
A:Title: A novel peptide, pyroglutamylglutaminylproline amide, in the rabbit prostate comp
A:Reference number: A33802; MUID:89255196; PMID:2498305
A:Accession: A33802
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <COC>
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 Q 1

RESULT 10
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocoulonum coulteri) (fragment)
C:Species: Gastrocoulonum coulteri
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterisation of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KIO>

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 2 Y 2

RESULT 11
PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N:Alternate names: ficus latex peptide 3
C:Species: Ficus carica (common fig)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PQ0010
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0010
A:Accession: PQ0010
A:Molecule type: protein
A:Residues: 1-3 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 L 1

RESULT 12
S13894
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: S13894
R:Nagal, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A:Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A:Reference number: S13894; MUID:91112783; PMID:1989490
A:Accession: S13894
A:Molecule type: protein
A:Residues: 1-3 <NAG>
A:Experimental source: var. capitata
C:Keywords: dimer; NAD; oxidoreductase

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 X 1
DB 1 X 1

RESULT 13
A43391
TRH-like tripeptide - alfalfa
C:Species: Medicago sativa (alfalfa)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A43391
R:Jackey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyrog
A:Reference number: A43391; MUID:92388092; PMID:1517203
A:Accession: A43391
A:Molecule type: protein
A:Residues: 1-3 <LAC>
C:Keywords: amidated carboxyl end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 2 Y 2

OY 1 x 1
DB 1 Q 1

RESULT 14

E37196
bradykinin-potentiating peptide 5 - Island Jararaca
C:Species: Bothrops insularis (Island Jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C:Accession: E37196
R:Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: E37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
C:Keywords: pyrrolidonic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 Q 1

RESULT 15

E37196
bradykinin-potentiating peptide 6 - Island Jararaca
C:Species: Bothrops insularis (Island Jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: E37196
R:Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: E37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
C:Keywords: pyrrolidonic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 Q 1

Search completed: May 7, 2003, 09:58:42
Job time : 3.36574 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:44:51 ; Search time 1.23148 Seconds

(without alignments)
235.760 Million cell updates/sec

Title: US-09-877-606-8

Perfect score: 7
Sequence: 1 XXXXXXX 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	0	0.0	3	1	GRWM_HUMAN
2	0	0.0	3	1	LOXE_VIBFI
3	0	0.0	3	1	THYL_PIG
4	0	0.0	4	1	ACH1_ACHFU
5	0	0.0	4	1	DCML_PSECH
6	0	0.0	4	1	DCML_PSECH
7	0	0.0	4	1	EOS1_HUMAN
8	0	0.0	4	1	FAR3_HIRME
9	0	0.0	4	1	FAR4_HIRME
10	0	0.0	4	1	FFRA_AMEL
11	0	0.0	4	1	FLRF_HIRME
12	0	0.0	4	1	FLRF_AMEL
13	0	0.0	4	1	FLRF_AMEL
14	0	0.0	4	1	FLRF_AMEL
15	0	0.0	4	1	FLRF_AMEL
16	0	0.0	4	1	FLRF_AMEL
17	0	0.0	4	1	FLRF_AMEL
18	0	0.0	4	1	FLRF_AMEL
19	0	0.0	4	1	FLRF_AMEL
20	0	0.0	4	1	FLRF_AMEL
21	0	0.0	4	1	FLRF_AMEL
22	0	0.0	4	1	FLRF_AMEL
23	0	0.0	4	1	FLRF_AMEL
24	0	0.0	4	1	FLRF_AMEL
25	0	0.0	4	1	FLRF_AMEL
26	0	0.0	4	1	FLRF_AMEL
27	0	0.0	4	1	FLRF_AMEL
28	0	0.0	4	1	FLRF_AMEL
29	0	0.0	4	1	FLRF_AMEL
30	0	0.0	4	1	FLRF_AMEL
31	0	0.0	4	1	FLRF_AMEL
32	0	0.0	4	1	FLRF_AMEL
33	0	0.0	4	1	FLRF_AMEL

34	0	0.0	5	1	TPIS_CANFA
35	0	0.0	5	1	TRM3_ECOLI
36	0	0.0	5	1	UC22_MAIZE
37	0	0.0	5	1	UP01_MOUSE
38	0	0.0	5	1	UXA4_CHLTR
39	0	0.0	6	1	ACPH_RABIT
40	0	0.0	6	1	ASP2_LACSN
41	0	0.0	6	1	CIP1_MYTEO
42	0	0.0	6	1	CIP2_MYTEO
43	0	0.0	6	1	EI01_LITRU
44	0	0.0	6	1	FARP_MONEX
45	0	0.0	6	1	LOK1_LOCM1

ALIGNMENTS

RESULT 1	GRWM_HUMAN	STANDARD;	PRT;	3 AA.
ID	GRWM_HUMAN			
AC	P01157;			
DT	21-JUL-1986 (rel. 01, Created)			
DT	21-JUL-1986 (rel. 01, Last sequence update)			
DT	21-JUL-1986 (rel. 01, Last annotation update)			
DE	Growth-modulating peptide.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE-77162369; PubMed-858356;			
RA	Schlesinger D.H., Pickart L., Thaler M.M.;			
RT	"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";			
RL	Experientia 33:324-325(1977). TRIPEPTIDE HAS BEEN FOUND TO STIMULATE			
CC	-1- MISCELLANEOUS: THIS SERUM AND TO INHIBIT OTHER TYPES IN VITRO.			
CC	GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.			
DR	PIR; A01421; GKHU.			
SO	SEQUENCE 3 AA; 340 MW; 6331E8100000000 CRC64;			
Query Match	Best Local Similarity	0.0%;	Score 0;	DB 1; Length 3;
Matches	0; Conservative	0;	Pred. No. 0;	
			Mismatches	1; Indels 0; Gaps 0;
OY	1 X 1			
DB	1 G 1			
RESULT 2	LOXE_VIBFI	STANDARD;	PRT;	3 AA.
ID	LOXE_VIBFI			
AC	P24272;			
DT	01-MAR-1992 (rel. 21, Created)			
DT	01-MAR-1992 (rel. 21, Last sequence update)			
DT	01-OCT-1996 (rel. 34, Last annotation update)			
DE	Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-			
DE	protein synthetase) (Fragment).			
GN	LOXE.			
OS	Vibrio fischeri.			
OC	Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.			
OX	NCBI_TaxID=668;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-91072226; PubMed-2254256;			
RA	Swartzman E., Kapoor S., Graham A.F., Meighan E.A.;			
RT	"A new Vibrio fischeri lux gene precedes a bidirectional termination			
RT	site for the lux operon.";			
RL	J. Bacteriol. 172:6797-6802(1990).			
CC	-1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.			
CC	IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE			
CC	FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS			
CC	SUBSTRATE IN THE LDCIFERASE-CATALYZED REACTION.			

CC -1- CATALYTIC ACTIVITY: AMP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -----
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 CC -----
 DR EMBL: M62812; -; NOT_ANNOTATED_CDS.
 DR Bioluminescence; Ligase.
 FT NON_TER 1
 SQ SEQUENCE 3 AA: 374 MW: 6AA3303000000000 CRC64;
 QY Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred.No. 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 0; Conservative 0;
 QY 1 X 1
 Db 1 1 1

RESULT 3
 ID THYL_PIG STANDARD; PRT; 3 AA.
 AC P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thyrolobin (Thyrotropin releasing hormone) (TRH) (Protirelin).
 OS Sus scrofa (Pig),
 OS Ovis aries (Sheep),
 OS Bombina orientalis (Oriental fire-bellied toad), and
 OS Neotrophthalmus viridescens (Eastern newt) (Triturus viridescens).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID:9823, 9940, 8346, 8316;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-Pig; TISSUE-Hypothalamus;
 RX MEDLINE-70136150; PubMed-4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone.";
 RL Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SYNTHESIS.
 RC SPECIES-Pig;
 RX MEDLINE-70039904; PubMed-4982117;
 RA Boier J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 RL releasing hormone and pyroglutanyl-histidyl-proline amide.";
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-Sheep; TISSUE-Hypothalamus;
 RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R.,
 RT "The elucidation of the primary structure of the hypothalamic thyroid
 RT stimulating hormone releasing factor of ovine origin by means of mass
 RT spectrometry.";
 RL Org. Mass Spectrom. 5:221-228(1971).
 RN [4]
 RP SYNTHESIS.
 RC SPECIES-Sheep;
 RX MEDLINE-70163386; PubMed-4985794;
 RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
 RT "Characterization of ovine hypothalamic hypophysiotropic
 RT TSH-releasing factor.";

RL Nature 226:321-325(1970).
 RN [5]
 RP SEQUENCE.
 RC SPECIES-Bombina orientalis; TISSUE-Skin;
 RX MEDLINE-76138399; PubMed-815011;
 RA Yasuhara T., Nakajima T.;
 RT "Letter: Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 RN [6]
 RP SEQUENCE.
 RC SPECIES-N. viridescens;
 RX MEDLINE-75035605; PubMed-4214528;
 RA Grimm-Joergensen Y., McKelvey J.F.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 RT viridescens) brain in vitro. Isolation and characterization of
 RT thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -1- FUNCTION: TRH FUNCTIONS AS A REGULATOR OF THE BIOSYNTHESIS OF TSH
 CC IN THE ANTERIOR PITUITARY GLAND AND AS A NEUROTRANSMITTER/
 CC NEUROMODULATOR IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS.
 CC
 CC PIR: A01415; RHEGT.
 DR PIR: A93750; RSHST.
 DR PIR: A90919; RHTDFO.
 DR PIR: A92971; A92971.
 KW Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 3 3 AMIDATION.
 SQ SEQUENCE 3 AA: 380 MW: 7761F6B000000000 CRC64;
 QY Query Match 0.0%; Score 0; DB 1; Length 3;
 Best Local Similarity 0.0%; Pred.No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 1 Q 1

RESULT 4
 ID ACH1_ACHFU STANDARD; PRT; 4 AA.
 AC P35904;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Achatina-I.
 OS Achatina fulica (Giant African snail).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 CC Achatinacea; Achatinidae; Achatina.
 OX NCBI_TaxID:6530;
 RN [1]
 RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN-Ferussac; TISSUE-Ganglion;
 RX MEDLINE-89273551; PubMed-2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
 RA Novales E.T., Kanadi C.G., Takeuchi H., Nomoto K.;
 RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Ferussac containing a D-amino acid residue.";
 RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2]
 RP CHARACTERIZATION.
 RC STRAIN-Ferussac; TISSUE-Heart atrium;
 RX MEDLINE-91264856; PubMed-1675568;
 RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function.";
 RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE-93014529; PubMed-1399265;
 RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,

RA Iwashita T., Nomoto K.;
 RT Crystal structure and molecular conformation of actinin-I
 (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 RT D-amino acid residue."
 RL Int. J. Pept. Protein Res. 39:258-264(1992).
 CC -1- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
 AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
 CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
 CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
 CC PIR: A32480; A32480.
 CC Hormone; D-amino acid.
 KW MOD_RES 2
 SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;
 QY Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 X 1
 DB 3 A 3

RESULT 5
 DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Bradyrhizobium group.
 CC NCBL_Taxid=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydophilic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: Molybdenum (molybdopterin).
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 CC PIR: PLO140; PLO140.
 CC Oxidoreductase; Molybdenum.
 KW NON_TER 4
 FT SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;
 QY Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 X 1
 DB 1 M 1

RESULT 6
 DCMS_PSECH STANDARD; PRT; 4 AA.
 AC P19918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO

DE dehydrogenase subunit S) (CO-DH S) (Fragment).
 GN CUTS.
 OS Pseudomonas carboxydohydrogena.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Bradyrhizobium group.
 CC NCBL_Taxid=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydophilic bacteria."
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 CC PIR: PLO146; PLO146.
 CC Oxidoreductase; Iron-sulfur.
 KW NON_TER 4
 FT SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;
 QY Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 X 1
 DB 2 A 2

RESULT 7
 EOSI_HUMAN STANDARD; PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Eosinophilic leucocyte peptides.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBL_Taxid=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76078412; PubMed=1060093;
 RA Goetzl E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilic tetrapeptides of
 RT human lung tissue: identification as eosinophil chemotactic factor of
 RT anaphylaxis."
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
 CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
 CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
 CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
 DR PIR: A03190; ETHUL.
 FT VARIANT 1
 FT SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;
 QY Query Match 0.0%; Score 0; DB 1; Length 4;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 X 1
 DB 3 S 3

RESULT 8
FAR3_HIRME STANDARD: PRT: 4 AA.
ID FAR3_HIRME
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
NX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsotis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 x 1
DB 1 y 1

RESULT 9
FAR4_HIRME STANDARD: PRT: 4 AA.
ID FAR4_HIRME
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
CC Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
NX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsotis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 x 1
DB 1 y 1

RESULT 10
FFKA_AMEL STANDARD: PRT: 4 AA.
ID FFKA_AMEL
AC P58705;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 x 1
DB 1 y 1

DE Antho-Kamide.
OS Euphyllura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nyantheae; Actinellidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Notackner H.-P., Rinehart K.L. Jr., Grimmelikhuijsen C.J.P.;
RT "Isolation of L-3-phenylactyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=83397415;
RA McFarlane I.D., Hudman D., Notackner H.-P., Grimmelikhuijsen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Ramide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1
FT MOD_RES 4
FT MOD_RES 4
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;
Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 x 1
DB 4 A 4

RESULT 11
FLRF_HIRME STANDARD: PRT: 4 AA.
ID FLRF_HIRME
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRFamide.
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudindae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsotis M.A., Calabrese R.L.;
RT "Identification of Rfamde neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RX SPECIES-H. trivolvis; TISSUE-Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."
RL Peptides 15:31-36(1994).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
FT MOD_RES 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
Query Match 0.0%; Score 0; DB 1; Length 4;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 F 1

RESULT 12

FLRN ANTEL STANDARD; PRT; 4 AA.
AC P58707;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Antho-Rhamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nynanthaeae; Actinellidae; Anthopleura.
OX NCBI_Taxid=6110;
RN [1]
RP SEQUENCE, AND MASS-SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Notack H.-P., Staley A.L.;
RT "Isolation of L-3-phenylactyl-Leu-Arg-Asn-NH2 (Antho-Rhamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
RT Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
RL -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FMAB.
KW Neuropeptide; Amidation.
FT MOD RES 1 1 L-3-PHENYLACTYL.
FT SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 F 1

RESULT 13

FMRF_MACNI STANDARD; PRT; 4 AA.
ID P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocallista nimbosa (Sun-ray clam).
OS Nerereis virens (Sandworm).
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchida; Veneroida;
OC Veneroidae; Veneridae; Macrocallista.
OX NCBI_Taxid=6594; 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197;670-671(1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RC SPECIES=M.nimbosa; TISSUE=ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;

RT "Purification and characterization of a cardioexcitatory neuropeptide
from the central ganglia of a bivalve mollusc.";
RT Prep. Biochem. 7:261-281(1977).
RN [3]
RP SEQUENCE.
RC SPECIES=N.virens;
RX MEDLINE=90259866; PubMed=2342992;
RA Krajinak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nerereis virens.";
RL Peptides 11:75-77(1990).
RN [4]
RP SEQUENCE.
RC SPECIES=H.medicalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Karlson M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [5]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -1- FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
ACTIVITIES INCLUDE AUGMENTATION, INDUCTION, AND REGULARIZATION OF
CARDIAC CONTRACTION.
CC -1- SIMILARITY: BELONGS TO THE FMRF (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
CC PIR: A01426; ECKN.
DR PIR: A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD RES 4 4 AMIDATION.
FT SEQUENCE 4 AA; 600 MW; 69D40699A000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

DB 1 F 1

RESULT 14

FMRF_MACNI STANDARD; PRT; 4 AA.
ID P58706;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Rhamide I [contains: Antho-Rhamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nynanthaeae; Actinellidae; Anthopleura.
OX NCBI_Taxid=6110;
RN [1]
RP SEQUENCE.
RC MEDLINE=92270459; PubMed=1821096;
RA Notack H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
biologically active L-3-phenylactyl-Tyr-Arg-Ile-NH2 and its
des-phenylactyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Notack H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-Rhamide and Antho-Rhamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron-specific.
DR InterPro: IPR001023; Hsp70.
KM Neuropeptide; Amidation.
FT CHAIN 1 4 ANTHO-RIAMIDE I.
FT CHAIN 2 4 ANTHO-RIAMIDE II.
FT MOD_RES 1 1 L-3-PHENYLACTYL.
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA: 598 MW: 60441B59A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 F 1

RESULT 15
OCPL_OCTMI STANDARD: PRT; 4 AA.
AC P58648;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides ocp-1/ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -1- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. ocp-2 is a 1000 time less
CC active than ocp-1.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: OCP-2 has L-Phe instead of D-Phe.
CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KM Hormone; D-amino acid.
FT MOD_RES 2 2 D-PHENYLTALANINE.
SQ SEQUENCE 4 AA: 394 MW: 6AAB79C810000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 G 1

Search completed: May 7, 2003, 09:54:40
Job time : 2.23148 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 5.02315 Seconds
(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-8
Perfect score: 7
Sequence: 1 xxxxxx 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-tyr:*
16: SP-bacteriap:*
17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	0	0.0	4	11	008433
2	0	0.0	5	2	P83073
3	0	0.0	5	10	Q99007
4	0	0.0	5	13	P83308
5	0	0.0	6	10	P82181
6	0	0.0	6	10	P82541
7	0	0.0	6	10	P82182
8	0	0.0	7	2	007354
9	0	0.0	7	2	047029
10	0	0.0	7	2	050556
11	0	0.0	7	2	034028
12	0	0.0	7	2	Q47477
13	0	0.0	7	2	Q47505
14	0	0.0	7	2	P70804
15	0	0.0	7	2	054248
16	0	0.0	7	2	P72081

17	0	0.0	7	4	Q15897
18	0	0.0	7	4	Q15903
19	0	0.0	7	5	P83374
20	0	0.0	7	6	Q28742
21	0	0.0	7	8	P92372
22	0	0.0	7	8	P92403
23	0	0.0	7	8	P92425
24	0	0.0	7	8	P92387
25	0	0.0	7	8	P92427
26	0	0.0	7	8	P92390
27	0	0.0	7	8	P92326
28	0	0.0	7	8	P92214
29	0	0.0	7	8	P92430
30	0	0.0	7	8	P92221
31	0	0.0	7	8	P92442
32	0	0.0	7	8	P92381
33	0	0.0	7	8	P92393
34	0	0.0	7	8	P92218
35	0	0.0	7	8	P92440
36	0	0.0	7	8	P92210
37	0	0.0	7	8	Q99182
38	0	0.0	7	8	Q95945
39	0	0.0	7	8	Q98866
40	0	0.0	7	8	P92421
41	0	0.0	7	8	P92385
42	0	0.0	7	10	Q49223
43	0	0.0	7	10	Q95583
44	0	0.0	7	10	P93233
45	0	0.0	7	10	P82445

ALIGNMENTS

RESULT 1
ID 008433 PRELIMINARY: PRT: 4 AA.
AC 008433;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-1999 (TREMBLrel. 09, Last annotation update)
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPCT)
DE (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H, Aono S, Kaishiyama S, Koike O;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -1- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND ENDOGENOUS COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
CC -1- BETA-D-GLUCURONOSIDE.
CC -1- SUBCELLULAR LOCATION: MICROsome.
CC EMBL; S38636; AAB19259.1; -;
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1
FT 4
SQ SEQUENCE 4 AA: 473 MW: 633732C420000000 CRC64;
Query Match 0.0%; Score 0; DB 11; Length 4;
Best local similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 x 1

DB 1 N 1

RESULT 2

P83073 PRELIMINARY; PRT; 5 AA.
 ID P83073
 AC P83073
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 CC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (Jul-2001) to the SWISS-PROT data bank.
 FT NON_TER
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA36F00000 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 4 T 4

RESULT 3

Q99007 PRELIMINARY; PRT; 5 AA.
 ID Q99007
 AC Q99007
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
 DE Alpha-amylase (EC 3.2.1.1) (Fragment).
 GN AMY1.
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER;
 RA MEDLINE-91329704; PubMed-1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellin
 RT acid and abscisic acid in protoplasts prepared from mature barley
 RT aleurone layers";
 RT Plant Mol. Biol. 16:713-721(1991).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
 CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
 CC -1- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
 CC -1- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
 CC BARLEY.
 DR EMBL: X54643; CA38455.1; -;
 KW Hydrolyase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
 KW Calcium; Multigene family.
 FT NON_TER
 SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 2 A 2

RESULT 4

P83308 PRELIMINARY; PRT; 5 AA.
 ID P83308
 AC P83308
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE FMRFamide-like neuropeptide (LPLRF-amide).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-BRAIN;
 RC PubMed-6137771;
 RX Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRFamide";
 RT Nature 305:328-330(1983).
 RL Nature 305:328-330(1983).
 CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide.
 SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 0.0%; Score 0; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 L 1

RESULT 5

P82181 PRELIMINARY; PRT; 6 AA.
 ID P82181
 AC P82181
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC STRAIN-CV. ALMARO; TISSUE-LEAF;
 RA MEDLINE-20435798; PubMed-10874046;
 RA Yamaguchi K., Sudrabanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the 50 S subunit of an organelle ribosome (chloroplast)";
 RT J. Biol. Chem. 275:28466-28482(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal L10.
 DR Pfam: PF00466; Ribosomal L10; PARTIAL.
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 6;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 A 1

RESULT 6

P82541 PRELIMINARY; PRT; 6 AA.
ID P82541
AC P82541
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Splachna oleracea (Splachn).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN-CV. ALMARO; TISSUE-LEAF.
RA MEDLINE=20435797; PubMed=10874039;
RT Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000)

CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MW=10477.0; METHOD-ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=10495; METHOD-MALDI.
CC -1- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
CC FORM IS THE MINOR BASIC FORM.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR002222; Ribosomal_S19.
DR Pfam: PF00203; Ribosomal_S19; PARTIAL.
DR PRINTS: PR00975; RIBOSOMAL_S19; PARTIAL.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 6;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 T 1

RESULT 7

P82182 PRELIMINARY; PRT; 6 AA.
ID P82182
AC P82182
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Splachna oleracea (Splachn).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN-CV. ALMARO; TISSUE-LEAF.
RA MEDLINE=20435798; PubMed=10874046;

Query Match 0.0%; Score 0; DB 10; Length 6;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC InterPro: IPR001790; Ribosomal_L10.
DR InterPro: IPR002363; Ribosomal_L10eub.
DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 0.0%; Score 0; DB 10; Length 6;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 A 1

RESULT 8

O07354 PRELIMINARY; PRT; 7 AA.
ID O07354
AC O07354
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE N1fk (Fragment).
GN N1fk.
OS Synecococcus sp. (strain PCC 8801 / RF-1) (Cyanothecae PCC 8801).
OC Bacteria; Cyanobacteria; Chroococcales; Cyanothecae.
OX NCBI_TaxID=41431;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RF-1;
RX MEDLINE=99231861; PubMed=10217509;
RA Huang T.C., Lin R.F., Chu M.K., Chen H.M.;
RT "Organization and expression of nitrogen-fixation genes in the aerobic
RT nitrogen-fixing unicellular cyanobacterium Synecococcus sp. strain
RT RF-1.";
RL Microbiology 145:743-753(1999).
DR EMBL: AF003700; AAC35193.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 849 MW; 7412C72A9D5B030 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 2 S 2

RESULT 9

O47029 PRELIMINARY; PRT; 7 AA.
ID O47029
AC O47029
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE AdA1 protein (Fragment).
OS Enterobacter cloacae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=550;

Query Match 0.0%; Score 0; DB 2; Length 7;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94079349; PubMed=8257126;
 RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
 RT "Analysis of the *aac(3)-Via* gene encoding a novel 3-N-
 RT acetyltransferase."
 RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
 DR EMBL; M88012; AAA16193.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 2 T 2

RESULT 10
 ID 050556 PRELIMINARY; PRT; 7 AA.
 AC 050556;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE GLYA (Fragment).
 GN GLYA.
 OS Actinobacillus actinomycetemcomitans (Haemophilus
 OS actinomycetemcomitans).
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Actinobacillus.
 OX NCBI_TaxID=714;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33384;
 RX MEDLINE=96355846; PubMed=8751884;
 RA Kolodrubetz D., Splitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
 RA Kreis E.;
 RT "cas Elements and trans factors are both important in strain-specific
 RT regulation of the leukotoxin gene in Actinobacillus
 RT actinomycetemcomitans."
 RL Infect. Immun. 64:3451-3460(1996).
 DR EMBL; U51862; AAB88721.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 7 A 7

RESULT 11
 ID 034028 PRELIMINARY; PRT; 7 AA.
 AC 034028;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Catechol-2,3-dioxygenase (Fragment).
 GN PHNE.
 OS Sphingomonas chungbukensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Sphingomonas.
 OX NCBI_TaxID=56193;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DJ77;

RA Kim Y.-C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88298; AAB6311.1; -.
 KW Dioxigenase.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 4 T 4

RESULT 12
 ID 047477 PRELIMINARY; PRT; 7 AA.
 AC 047477;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE Tpl protein (Fragment).
 GN Tpl.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 RP SEQUENCE OF 7-7 FROM N.A.
 RX MEDLINE=85203917; PubMed=3158524;
 RA Hellinga H.W., Evans P.R.;
 RT "Nucleotide sequence and high-level expression of the major
 RT Escherichia coli phosphotransferase."
 RL Eur. J. Biochem. 149:363-373(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Evans P.;
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X02519; CAA26359.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 A 1

RESULT 13
 ID 047505 PRELIMINARY; PRT; 7 AA.
 AC 047505;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Mcca protein.
 GN MCCA.
 OS Escherichia coli.
 OG Plasmid pmcc7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96099297; PubMed=8522520;
 RA Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
 RT "Structure and organization of Plasmid genes required to produce the
 RT translation inhibitor microcin C7."

RL J. Bacteriol. 177:7131-7140(1995).
 DR EMBL; X57583; CAA40808.1; -.
 KW Plasmid.
 SQ SEQUENCE 7 AA; 763 MW; 644DD44861B406F0 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 3 T 3

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 2 T 2
 Search completed: May 7, 2003, 09:57:22
 Job time : 6.02315 secs

RESULT 14
 P70804 PRELIMINARY; PRT; 7 AA.
 ID P70804;
 AC P70804;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Algt protein (Fragment).
 GN Algt.
 OS Azotobacter vinelandii.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Azotobacter.
 OX NCBI_TaxID=354;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E;
 RX MEDLINE=96427318; PubMed=8830682;
 RA Rehm B.H.A., Ertesvag H., Valla S.;
 RT "A new Azotobacter vinelandii manuronan C-5-epimerase gene (algt) is
 RT part of an algt gene cluster physically organized in a manner similar
 RT to that in Pseudomonas aeruginosa.";
 RL J. Bacteriol. 178:5884-5889(1996).
 DR EMBL; X67973; CAA61230.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 684 MW; 71B5A5A2D1AED0 CRC64;

Query Match 0.0%; Score 0; DB 2; Length 7;
 Best Local Similarity 0.0%; Pred. No. 0;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 X 1
 Db 2 T 2

RESULT 15
 O54248 PRELIMINARY; PRT; 7 AA.
 ID O54248;
 AC O54248;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE RplO protein (Fragment).
 GN RplO.
 OS Streptomyces griseus.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RX MEDLINE=20011291; PubMed=10542330;
 RA Pehling S., Piepersberg W., Wehmeier U.F.;
 RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
 RT N2-3-11 and interaction of the sec Y protein with the SecA protein.";
 RL Biochim. Biophys. Acta 1447:298-302(1999).
 DR EMBL; X95915; CAA65160.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 2.07407 Seconds
(without alignments)
99.302 Million cell updates/sec

Title: US-09-877-606-8

Perfect score: 7
Sequence: 1 xxxxxx 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	1	US-07-820-154A-12
2	0	0.0	1	1	US-07-791-213D-24
3	0	0.0	1	1	US-07-791-213D-40
4	0	0.0	1	1	US-08-174-365A-57
5	0	0.0	1	1	US-07-789-913-23
6	0	0.0	1	1	US-07-789-913-25
7	0	0.0	1	1	US-08-049-794-23
8	0	0.0	1	1	US-08-049-794-25
9	0	0.0	1	1	US-08-433-037-12
10	0	0.0	1	1	US-08-448-606-4
11	0	0.0	1	1	US-07-869-933-16
12	0	0.0	1	1	US-08-293-150A-24
13	0	0.0	1	1	US-08-293-150A-40
14	0	0.0	1	1	US-08-496-847-23
15	0	0.0	1	1	US-08-496-847-25
16	0	0.0	1	1	US-08-742-774-23
17	0	0.0	1	1	US-08-742-774-25
18	0	0.0	1	1	US-08-675-354-23
19	0	0.0	1	1	US-08-675-354-25
20	0	0.0	1	1	US-08-097-554A-12
21	0	0.0	1	1	US-08-965-918-23
22	0	0.0	1	1	US-08-965-918-25
23	0	0.0	1	1	US-09-138-439-23
24	0	0.0	1	1	US-09-138-439-25
25	0	0.0	1	1	US-08-480-640A-12
26	0	0.0	1	1	US-08-613-400A-23
27	0	0.0	1	3	US-08-613-400A-25

28	0	0.0	1	3	US-08-801-092-10	Sequence 10, Appl
29	0	0.0	1	3	US-08-801-092-17	Sequence 17, Appl
30	0	0.0	1	3	US-08-801-092-24	Sequence 24, Appl
31	0	0.0	1	3	US-08-801-092-31	Sequence 31, Appl
32	0	0.0	1	3	US-08-801-092-38	Sequence 38, Appl
33	0	0.0	1	3	US-08-801-092-45	Sequence 45, Appl
34	0	0.0	1	3	US-09-298-017-23	Sequence 23, Appl
35	0	0.0	1	3	US-09-298-017-25	Sequence 25, Appl
36	0	0.0	1	3	US-08-295-802-12	Sequence 12, Appl
37	0	0.0	1	4	US-09-392-979A-23	Sequence 23, Appl
38	0	0.0	1	4	US-09-392-979A-25	Sequence 25, Appl
39	0	0.0	1	4	US-09-103-663-16	Sequence 16, Appl
40	0	0.0	1	4	US-08-488-237A-12	Sequence 12, Appl
41	0	0.0	1	4	US-09-117-927-5	Sequence 5, Appl
42	0	0.0	1	4	US-08-375-992A-12	Sequence 12, Appl
43	0	0.0	1	4	US-09-315-113-10	Sequence 10, Appl
44	0	0.0	1	4	US-09-315-113-17	Sequence 17, Appl
45	0	0.0	1	4	US-09-315-113-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-07-820-154A-12
Sequence 12, Application US/07820154A
Patent No. 5382425
GENERAL INFORMATION:
APPLICANT: Cochran Ph.D., Mark D
APPLICANT: Junker M.S., David E
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,154A
FILING DATE: 19920113
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-07-820-154A-12
Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
Db 1 V 1
RESULT 2
US-07-791-213D-24

Sequence 24, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-24
Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 C 1
RESULT 3
US-07-791-213D-40
Sequence 40, Application US/07791213D
Patent No. 5409895
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshiro
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States

ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07791,213D
FILING DATE: 13-NOV-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-791-213D-40
Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 X 1
DB 1 C 1
RESULT 4
US-08-174-365A-57
Sequence 57, Application US/08174365A
Patent No. 5478809
GENERAL INFORMATION:
APPLICANT: Seilich TANIDA et al.
TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08174,365A
FILING DATE: December 28, 1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified site
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note = "Xaa is modified amino acid as
OTHER INFORMATION: described in specification"
US-08-174-365A-57

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1
DB 1 X 1

RESULT 5
US-07-789-913-23
Sequence 23, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO

ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-23

Query Match
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 C 1

RESULT 6
US-07-789-913-25
Sequence 25, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:
APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.
TITLE OF INVENTION: Delayed Treatment Method of Reducing
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,913
FILING DATE: 19911112
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/561,766
FILING DATE: 02-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/440,094
FILING DATE: 22-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0005.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: both
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-25

Query Match
Best Local Similarity 0.0%; Score 0; DB 1; Length 1;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 R 1

RESULT 7
US-08-049-794-23; Sequence 23, Application US/08049794
; Patent No. 5587454

GENERAL INFORMATION:

APPLICANT: JUSTICE, ALAN

APPLICANT: SINGH, TEJINDER

APPLICANT: GOHIL, KISHOR C

APPLICANT: VALENTINO, KAREN L

APPLICANT: MILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/049,794

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0960

TELEFAX: (415) 324-0880

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acids

TYPE: AMINO ACID

TOPOLOGY: Linear

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE

INDIVIDUAL ISOLATE: 32

US-08-049-794-23

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 X 1

Db 1 R 1

RESULT 8
US-08-049-794-25

; Sequence 25, Application US/08049794

; Patent No. 5587454

GENERAL INFORMATION:

APPLICANT: JUSTICE, ALAN

APPLICANT: SINGH, TEJINDER

APPLICANT: GOHIL, KISHOR C

APPLICANT: VALENTINO, KAREN L

APPLICANT: MILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

APPLICANT: MILJANICH, GEORGE P

TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/049,794

APPLICATION NUMBER: US/08/049,794

FILING DATE: 19930415

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/814,759

FILING DATE: 30-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0960

TELEFAX: (415) 324-0880

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1 amino acids

TYPE: AMINO ACID

TOPOLOGY: Linear

MOLECULE TYPE: Protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE

INDIVIDUAL ISOLATE: 32

US-08-049-794-25

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 X 1

Db 1 R 1

RESULT 9
US-08-433-037-12

; Sequence 12, Application US/08433037

; Patent No. 5707828

GENERAL INFORMATION:

APPLICANT: Sreekrishna, Kotikanyadan

APPLICANT: Barr, Kathryn A.

APPLICANT: Brietley, Russell A.

APPLICANT: Thill, Gregory P.

APPLICANT: Tschopp, Ueerg F.

TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: U.S.A.

ZIP: 11530-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-037-12

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 L 1

RESULT 10
US-08-448-606-4
Sequence 4, Application US/08448606
Patent No. 572114
GENERAL INFORMATION:
APPLICANT: Abrahams n, Lars
APPLICANT: Holmgren, Erik
APPLICANT: Kaider n, Christina
APPLICANT: Lake, Mats
APPLICANT: Mikaelsson, sa
APPLICANT: Sejlitz, Torsten
TITLE OF INVENTION: Expression System For Producing
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: Pollock, Vande Sande & Priddy
STREET: 1990 M Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,606
FILING DATE: 25-AUG-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE93/01061
FILING DATE: 09-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9203753-0
FILING DATE: 11-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Amerinick, Burton A.
REGISTRATION NUMBER: 24,852
REFERENCE/DOCKET NUMBER: 0151/00121
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)331-7111
TELEFAX: (202) 293-6229
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-606-4

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 Q 1

RESULT 11
US-07-869-933-16
Sequence 16, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHID
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-869-933-16

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
DB 1 M 1

RESULT 12
US-08-293-150A-24
Sequence 24, Application US/08293150A

Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-24

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 C 1

RESULT 13
US-08-293-150A-40
Sequence 40, Application US/08293150A
Patent No. 5792629
GENERAL INFORMATION:
APPLICANT: MORISHITA, Hideaki
APPLICANT: KANAMORI, Toshinori
APPLICANT: NOBUHARA, Masahiro
TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
TITLE OF INVENTION: TREATING USING THE SAME
NUMBER OF SEQUENCES: 110
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-40

STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,150A
FILING DATE: 19-AUG-1994
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/791,213
FILING DATE: 13-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-306745
FILING DATE: 13-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 029650-049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-6620
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-150A-40

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 C 1

RESULT 14
US-08-496-847-23
Sequence 23, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A

REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-23

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 x 1
DB 1 c 1

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 x 1
DB 1 R 1

Search completed: May 7, 2003, 09:59:52
Job time: 3.07407 secs

RESULT 15
US-08-496-847-25
Sequence 25, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-25
Query Match 0.0%; Score 0; DB 1; Length 1;

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 3.85648 Seconds

(without alignments)
167.038 Million cell updates/sec

Title: US-09-877-606-8

Perfect score: 7

Sequence: 1 xxxxxxx 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCY_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCYUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	1	9 US-10-024-860-4	Sequence 4, Appl1
2	0	0.0	1	9 US-09-809-391-395	Sequence 395, App
3	0	0.0	1	9 US-09-809-391-611	Sequence 46, Appl
4	0	0.0	1	9 US-10-226-956-279	Sequence 279, App
5	0	0.0	1	10 US-09-909-348-4	Sequence 4, Appl1
6	0	0.0	1	10 US-09-982-172-3	Sequence 3, Appl1
7	0	0.0	1	10 US-09-982-172-4	Sequence 4, Appl1
8	0	0.0	1	10 US-09-982-172-9	Sequence 11, Appl1
9	0	0.0	1	10 US-09-982-172-11	Sequence 9, Appl1
10	0	0.0	1	10 US-09-982-172-19	Sequence 31, Appl1
11	0	0.0	1	10 US-09-982-172-31	Sequence 35, Appl1
12	0	0.0	1	10 US-09-982-172-35	Sequence 37, Appl1
13	0	0.0	1	10 US-09-982-172-37	Sequence 46, Appl1
14	0	0.0	1	10 US-09-982-172-46	Sequence 69, Appl1
15	0	0.0	1	10 US-09-982-172-69	Sequence 80, Appl1
16	0	0.0	1	10 US-09-982-172-80	Sequence 81, Appl1
17	0	0.0	1	10 US-09-982-172-81	Sequence 83, Appl1
18	0	0.0	1	10 US-09-982-172-83	Sequence 86, Appl1
19	0	0.0	1	10 US-09-982-172-86	Sequence 86, Appl1

20	0	0.0	1	10 US-09-982-172-93	Sequence 93, Appl1
21	0	0.0	1	10 US-09-982-172-95	Sequence 95, Appl1
22	0	0.0	1	10 US-09-982-172-106	Sequence 106, App
23	0	0.0	1	10 US-09-982-172-112	Sequence 112, App
24	0	0.0	1	10 US-09-982-172-120	Sequence 120, App
25	0	0.0	1	10 US-09-982-172-126	Sequence 126, App
26	0	0.0	1	10 US-09-982-172-148	Sequence 148, App
27	0	0.0	1	10 US-09-982-172-149	Sequence 149, App
28	0	0.0	1	10 US-09-982-172-155	Sequence 155, App
29	0	0.0	1	10 US-09-982-172-160	Sequence 160, App
30	0	0.0	1	10 US-09-982-172-173	Sequence 172, App
31	0	0.0	1	10 US-09-982-172-177	Sequence 173, App
32	0	0.0	1	10 US-09-982-172-175	Sequence 175, App
33	0	0.0	1	10 US-09-982-172-189	Sequence 189, App
34	0	0.0	1	10 US-09-982-172-190	Sequence 190, App
35	0	0.0	1	10 US-09-982-172-191	Sequence 191, App
36	0	0.0	1	10 US-09-982-172-195	Sequence 195, App
37	0	0.0	1	10 US-09-982-172-200	Sequence 200, App
38	0	0.0	1	10 US-09-982-172-211	Sequence 211, App
39	0	0.0	2	9 US-09-554-000-52	Sequence 52, Appl1
40	0	0.0	2	9 US-09-887-853-9	Sequence 9, Appl1
41	0	0.0	2	9 US-10-061-395-70	Sequence 70, Appl1
42	0	0.0	2	9 US-10-005-438-3	Sequence 3, Appl1
43	0	0.0	2	9 US-10-119-417-16	Sequence 16, Appl1
44	0	0.0	2	9 US-09-809-391-546	Sequence 546, App
45	0	0.0	2	9 US-09-836-433-15	Sequence 15, Appl1

ALIGNMENTS

RESULT 1
US-10-024-860-4 Application US/10024860
; Sequence 4, Application US/10024860
; Patient No. US20020172692A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Joseph
; TITLE OF INVENTION: Vaccine Composition Against Malaria
; FILE REFERENCE: B45088C2
; CURRENT APPLICATION NUMBER: US/10/024,860
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 09/826,513
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 09/230,629
; PRIOR FILING DATE: 1999-01-26
; PRIOR APPLICATION NUMBER: GB 9616351.4
; PRIOR FILING DATE: 1996-08-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Hepatitis B
US-10-024-860-4

Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 x 1
DB 1 R 1

RESULT 2
US-09-809-391-395
; Sequence 395, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P200292
; CURRENT APPLICATION NUMBER: US/09/809,391

;; CURRENT FILING DATE: 2001-03-16
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 761
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 395
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-809-391-395

Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
Db 1 M 1

RESULT 3
US-09-809-391-611
;; Sequence 611, Application US/09809391
;; Publication No. US20030049618A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: 186 Human Secreted proteins
;; FILE REFERENCE: P2002P2
;; CURRENT APPLICATION NUMBER: US/09/809,391
;; CURRENT FILING DATE: 2001-03-16
;; Prior application data removed - consult PALM or file wrapper
;; NUMBER OF SEQ ID NOS: 761
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO 611
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-809-391-611

Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
Db 1 M 1

RESULT 4
US-10-226-956-279
;; Sequence 279, Application US/10226956
;; Publication No. US20030060399A1
;; GENERAL INFORMATION:
;; APPLICANT: Brophy, Colleen
;; APPLICANT: Komalavillas, Padmini
;; APPLICANT: Panitch, Alyssa
;; APPLICANT: Joshi, Lokesh
;; APPLICANT: Seal, Brandon L.
;; TITLE OF INVENTION: REAGENTS AND METHODS FOR SMOOTH MUSCLE THERAPIES
;; FILE REFERENCE: ASU-1061-US
;; CURRENT APPLICATION NUMBER: US/10/226,956
;; CURRENT FILING DATE: 2002-08-23
;; PRIOR APPLICATION NUMBER: 60/314,535
;; PRIOR FILING DATE: 2001-08-23
;; NUMBER OF SEQ ID NOS: 320
;; SOFTWARE: Patentln version 3.1
;; SEQ ID NO 279
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic peptide
NAME/KEY: MISC_FEATURE

;; LOCATION: (1)..(1)
;; OTHER INFORMATION: X 1s (R)4-9
US-10-226-956-279

Query Match 0.0%; Score 0; DB 9; Length 1;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 X 1
Db 1 M 1

RESULT 5
US-09-909-348-4
;; Sequence 4, Application US/09909348
;; Patent No. US20020042373A1
;; GENERAL INFORMATION:
;; APPLICANT: Carney, Darrell H.
;; APPLICANT: Crowther, Roger S.
;; APPLICANT: Stierberg, Janet
;; APPLICANT: Bergmann, John
;; TITLE OF INVENTION: Stimulation of Cartilage Growth With Agonists
;; FILE REFERENCE: 3033.1003-001
;; CURRENT APPLICATION NUMBER: US/09/909,348
;; CURRENT FILING DATE: 2001-07-19
;; PRIOR APPLICATION NUMBER: US 60/219,800
;; PRIOR FILING DATE: 2000-07-20
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4
;; LENGTH: 14
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide fragment of Thrombin
NAME/KEY: VARIANT
LOCATION: (1)..(14)
;; OTHER INFORMATION: Xaa at position six is Glu or Gln
;; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or
US-09-909-348-4

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1
Db 1 V 1

RESULT 6
US-09-982-172-3
;; Sequence 3, Application US/09982172
;; Patent No. US20020137119A1
;; GENERAL INFORMATION:
;; APPLICANT: Email Israel Katz
;; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBIO
;; TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENE
;; TITLE OF INVENTION: UTILIZING EACH
;; FILE REFERENCE: 01/22283
;; CURRENT APPLICATION NUMBER: US/09/982,172
;; CURRENT FILING DATE: 2001-10-19
;; NUMBER OF SEQ ID NOS: 253
;; SOFTWARE: Patentln version 3.1
;; SEQ ID NO 3
;; LENGTH: 1
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-3

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 K 1

RESULT 7
US-09-982-172-4
; Sequence 4, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 K 1

RESULT 8
US-09-982-172-9
; Sequence 9, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-9

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 K 1

RESULT 9

US-09-982-172-11
; Sequence 11, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 K 1

RESULT 10
US-09-982-172-19
; Sequence 19, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-19

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 x 1
DB 1 K 1

RESULT 11
US-09-982-172-31
; Sequence 31, Application US/09982172
; Patent No. US20020137119A1
; GENERAL INFORMATION:
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAL
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19

NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 1
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-31

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 12
US-09-982-172-35
Sequence 35, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERAL
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 1
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-35

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 R 1

RESULT 13
US-09-982-172-37
Sequence 37, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERAL
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 1
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-37

Query Match 0.0%; Score 0; DB 10; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 14
US-09-982-172-46
Sequence 46, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERAL
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46
LENGTH: 1
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-46

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

RESULT 15
US-09-982-172-69
Sequence 69, Application US/09982172
Patent No. US20020137119A1
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
TITLE OF INVENTION: DIRECTED THERAGAINS, AND METHODS, SYSTEMS AND KITS FOR GENERAL
FILE REFERENCE: 01/22283
CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PatentIn version 3.1
SEQ ID NO 69
LENGTH: 1
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-69

Query Match 0.0%; Score 0; DB 10; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 K 1

Search completed: May 7, 2003, 10:21:55
Job time : 3.85648 secs

PT Production of constrained helical peptide(s) by linking side chains
 PT on termini of octa-peptide - derived from human immunodeficiency
 PT virus gp41 protein, useful in vaccines for treatment and prevention
 PT of infection
 PS Claim 11, Page 156; 279pp; English.
 XX
 CC Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
 CC (HIV). Specifically, AAY22810-Y22910 are derived from gp41 proteins
 CC of known HIV virus strains (AAY22810, AAY22871, AAY22880, AAY22888 and
 CC AAY22903 represent consensus sequences of various sections of the gp41
 CC protein). Sequences derived from the peptides are used to produce
 CC constrained helical peptides of the invention. The constrained helical
 CC peptide is produced by synthesizing an octapeptide in which both terminal
 CC amino acids have a side-chain that includes a group able to form an amide
 CC bond, and cyclizing the octapeptide by reacting the specified side-chain
 CC residues with a difunctional linker to produce two amide bonds.
 CC The constrained helical peptides are used to treat or prevent HIV
 CC infection, especially as vaccines that generate antibodies that
 CC prevent viral membrane fusion or infectivity. Vaccines may contain
 CC constrained helical peptides derived from several different strains of
 CC HIV. The antibodies are also useful for diagnosing HIV infection. Other
 CC uses for the constrained helical peptides are in affinity purification
 CC of ligands (particularly where complete binding protein is not readily
 CC available), e.g. replacements for protein A in immunoglobulin
 CC purification), as epitope mimics for antibody production, for isolation
 CC of synthetic antibody clones from phage display libraries, or as stable
 CC forms of "floppy" peptides or proteins.
 CC
 SQ Sequence 268 AA;
 Query Match 96.9%; Score 281; DB 19; Length 268;
 Best Local Similarity 96.2%; Pred. No. 3,1e-22;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHTTWMEMREINNTSLIHSIESQNOEKLEDELLELDKWSLMMWFI 52
 DB 154 NHTTWMEMREINNTSLIHSIESQNOEKNEQELLELDKWSLMMWFI 205
 RESULT 2
 ABG68291
 ID ABG68291 standard; Protein; 268 AA.
 XX
 AC ABG68291;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Envelope protein gp41 from HIV clade B strain #10.
 XX
 KM HIV, glycoprotein; gp41; antigen; helical conformation;
 KM virus-induced membrane fusion; acquired immunodeficiency syndrome; AIDS;
 KM viral envelope protein; vaccine; virucide; anti-HIV.
 XX
 OS Human immunodeficiency virus type 1 clade B.
 XX
 PN US6271198-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 05-NOV-1997; 97US-0965056.
 XX
 PR 16-JUN-1997; 97US-049787P.
 PR 06-NOV-1996; 96US-0743698.
 PR 16-JUN-1997; 97US-0876698.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Braisted AC, Judice JK, McDowell RS, Phelean JC, Starovasnik MA;
 PI Wells JA;
 XX
 DR WPI; 2002-487624/52.
 XX

PT New cyclic peptides from human immune deficiency virus gp41, useful for
 PT treatment or prevention of HIV infection, are constrained to have
 PT alpha-helical conformation
 PS Disclosure; Column 151-154; 175pp; English.
 XX
 CC The invention relates to cyclic peptides (A) with a constrained helical
 CC conformation, derived from gp41 (glycoprotein 41, a viral envelope
 CC protein) of human immunodeficiency virus (HIV). The cyclic
 CC peptides have formulas given in the specification part of which are
 CC derived from a consensus sequence of gp41 derived from HIV clades A, B,
 CC C, D, E or O. The peptides are used to cause induction of a specific
 CC immune response, resulting in antibodies that prevent virus-induced
 CC membrane fusion. The peptides are used to treat subjects with, or at risk
 CC of, HIV infection, either as antilution/anti-infection agents or,
 CC preferably where associated with a carrier, as an immunogen (including as
 CC vaccine) to raise antibodies. The antibodies may be used for diagnosis or
 CC prevention/treatment of HIV infection (i.e. acquired immunodeficiency
 CC syndrome, AIDS), e.g. prevention of mother-to-child transmission or in
 CC cases of health care accidents. The peptides can be based on specific HIV
 CC strains, e.g. breakthrough isolates of HIV that have developed during
 CC vaccine trials, so a combination of them should cover a wide range of
 CC protection. The present sequence is gp41 protein from a particular
 CC HIV clade used to derive a consensus sequence of gp41.
 CC
 SQ Sequence 268 AA;
 Query Match 96.9%; Score 281; DB 23; Length 268;
 Best Local Similarity 96.2%; Pred. No. 3,1e-22;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NHTTWMEMREINNTSLIHSIESQNOEKLEDELLELDKWSLMMWFI 52
 DB 154 NHTTWMEMREINNTSLIHSIESQNOEKNEQELLELDKWSLMMWFI 205
 RESULT 3
 ABB83400
 ID ABB83400 standard; Protein; 344 AA.
 XX
 AC ABB83400;
 XX
 DT 19-SEP-2002 (first entry)
 XX
 DE HIV gp41 LAI protein #1.
 XX
 KM HIV, gp41; LAI; virucide; anti-HIV; vaccine; HIV infection.
 XX
 OS Human immunodeficiency virus.
 XX
 FH Key
 FH Peptide 1..23
 FT Location/Qualifiers
 FT /Label= Fusion_peptide
 FT 173..194
 FT Domain /Label= Transmembrane_domain
 XX
 PN WO200253587-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 04-JAN-2002; 2002WO-FR00031.
 XX
 PR 05-JAN-2001; 2001FR-0000141.
 PR 23-JAN-2001; 2001FR-0000848.
 XX
 PA (AVET) AVENTIS PASTEUR.
 XX
 PI Brasseur R, Charlotiaux B, Chevallier M, El Habib R, Krell T;
 PI Sodoyer R;
 XX
 DR WPI; 2002-528852/56.
 XX
 PT New mutant human immune deficiency virus gp41 polypeptide, useful in

[illegible]

```

CC      stop codon in AAG66275.
XX
SQ      Sequence      420 AA:

Query Match      96.9%; Score 281; DB 15; Length 420;
Best Local Similarity 96.2%; Pred. No. 5,1e-22;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0.

OY      1 NHTTWLEMDREINNTYSLIHSIIIESQNOQEKLEDELLLELDKWSIWMNFNI 52
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DB      155 NHTTWLEMDREINNTYSLIHSIIIESQNOQEKNEDELLLELDKWSIWMNFNI 206

RESULT 5
ID      AAM00181 standard; Protein; 519 AA.
XX
AC      AAM00181;
XX
DT      12-NOV-1996 (first entry)
XX
DE      HIV-1 env protein.
XX
KW      Poliovirus; encapsidation; capsid; vaccine; genetic immunisation;
KM      HIV-1; human immunodeficiency virus type 1; env protein.
XX
OS      Human immunodeficiency virus type 1.
XX
PN      MO9625173-A1.
XX
PD      22-AUG-1996.
XX
PE      13-FEB-1996; 96WO-US01895.
XX
PR      15-FEB-1995; 95US-0389459.
XX
PA      (UABR-) UAB RES FOUND.
XX
PI      Ansaard DC, Morrow CD, Porter DC;
XX
WPI: 1996-393136/39.
XX
N-PSDB: AAT33295.
XX
PT      Encapsidation of recombinant polio:virus nucleic acid for use in
PT      vaccines - using a polio:virus nucleic acid which lacks the p1
PT      capsid region and an expression system which provides the region
XX
PS      Disclosure; Page 61-63; 108bp; English.
XX
CC      cDNA sequences (AAT33293-95) respectively code for the gag, pol and
CC      env proteins (AAM00179-81) of HIV-1. They can be used to substitute
CC      the p1 capsid gene of poliovirus in recombinant poliovirus nucleic
CC      acids (rPNAs). Such rPNAs are encapsidated by introduction into
CC      a host cell together with a vaccinia virus or plasmid vector
CC      encoding the poliovirus p1 capsid precursor protein. Encapsidated
CC      rPNAs are useful for genetic immunisation, stimulating an immune
CC      response to the HIV-1 protein.
XX
SQ      Sequence      519 AA:

Query Match      96.9%; Score 281; DB 17; Length 519;
Best Local Similarity 96.2%; Pred. No. 6,5e-22;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0.

OY      1 NHTTWLEMDREINNTYSLIHSIIIESQNOQEKLEDELLLELDKWSIWMNFNI 52
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      420 NHTTWLEMDREINNTYSLIHSIIIESQNOQEKNEDELLLELDKWSIWMNFNI 471

RESULT 6
ID      AAR69997 standard; Protein; 521 AA.
XX

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AC AAR69997;
 XX
 DT 13-SEP-1995 (first entry)
 XX
 DE HIV-1 env protein.
 XX
 KM Encapsulation; Human immunodeficiency virus; type 1; immunogenic;
 KM poliovirus.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN CA2125344-A.
 XX
 PD 02-JAN-1995.
 XX
 PF 07-JUN-1994; 94CA-2125344.
 XX
 PR 01-JUL-1993; 93US-0087009.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Morrow CD;
 XX
 DR WPI: 1995-099021/14.
 DR N-PSDB: AA080573.
 XX
 PT Method for encapsulating recombinant polio:virus nucleic acid -
 XX useful for providing comps. to stimulate immune response.
 PS Disclosure; Page 38; 62pp; English.
 CC
 CC The sequence is that of the HIV-1 env protein. The DNA encoding
 CC such protein is used in a method (claimed) to encapsulate
 CC poliovirus cDNA to make it more immunogenic.
 CC See also AAR69995-6.
 XX
 SQ Sequence 521 AA;
 Query Match 96.9%; Score 281; DB 16; Length 521;
 Best Local Similarity 96.2%; Pred. No. 6.5e-22;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NHTTWEMREINNTSLHSLSIESQNOEKLEQELLEDKRWASLWNFNI 52
 DB 420 NHTTWEMREINNTSLHSLSIESQNOEKNEQELLEDKRWASLWNFNI 471
 RESULT 7
 AAM43066
 ID AAM43066 standard; peptide; 853 AA.
 XX
 AC AAM43066;
 XX
 DT 11-SEP-1998 (first entry)
 XX
 DE HIV-1 gp120 protein fragment from isolate HXB2.
 XX
 KM gp120 protein; purification; fractionation; ion exchange; chromatography;
 KM binding affinity; CD4; hydrophobic interaction; size exclusion; vaccine.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN US5696238-A.
 XX
 PD 09-DEC-1997.
 XX
 PF 11-MAY-1995; 95US-0439286.
 XX
 PR 20-AUG-1991; 91US-0684963.
 PR 16-AUG-1993; 93US-0109002.
 PR 09-MAY-1994; 94US-0240073.
 PR 11-MAY-1995; 95US-0439286.
 XX

PA (CHIR) CHIRON CORP.
 XX
 PI Haigwood NL, Scandella C;
 XX
 DR WPI: 1998-041353/04.
 XX
 PT Purification of HIV gp120 - using chromatographic methods
 XX
 PS Disclosure; Fig 2A-W; 53pp; English.
 XX
 CC AAM43066-M43080 are fragments of the gp120 protein from different human
 CC immunodeficiency virus type 1 (HIV-1) isolates. These proteins are used
 CC in a novel method for purifying HIV gp120 so as to provide a purified
 CC gp120 glycoprotein having protein/protein binding properties
 CC substantially identical to natural viral HIV gp120. The method involves
 CC fractionating a crude gp120 preparation containing full-length,
 CC glycosylated gp120 using ion exchange chromatography so as to provide a
 CC first collection of fractions. A fraction from the first collection is
 CC selected that exhibits specific binding affinity for CD4 peptide,
 CC thereby producing a first fractionated material. The first fractionated
 CC material is fractionated by hydrophobic interaction chromatography so as
 CC to provide a second collection of fractions from which a second
 CC collection is selected that exhibits specific binding affinity for CD4
 CC peptide. This second fraction is fractionated by size exclusion
 CC chromatography so as to provide a third collection of fractions
 CC exhibiting specific binding affinity for CD4 peptide, thereby providing
 CC the purified gp120. The purified gp120 can be used for antibody
 CC production and in vaccines.
 XX
 SQ Sequence 853 AA;
 Query Match 96.9%; Score 281; DB 19; Length 853;
 Best Local Similarity 96.2%; Pred. No. 1.1e-21;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 NHTTWEMREINNTSLHSLSIESQNOEKLEQELLEDKRWASLWNFNI 52
 DB 621 NHTTWEMREINNTSLHSLSIESQNOEKNEQELLEDKRWASLWNFNI 672
 RESULT 8
 AAP60131
 ID AAP60131 standard; Protein; 856 AA.
 XX
 AC AAP60131;
 XX
 DT 26-JUN-1991 (first entry)
 XX
 DE Sequence of the AIDS envelope protein.
 XX
 KM AIDS; HIV; LAV; HTLV-III; vaccine; antibody; epitope; antigen;
 KM diagnosis.
 XX
 OS HTLV-III.
 XX
 PN EP199301-A.
 XX
 PD 29-OCT-1986.
 XX
 PF 18-APR-1986; 86EP-0105371.
 XX
 PR 19-APR-1985; 85US-0725021.
 XX
 PA (HOPE) HOFFMANN-LA ROCHE AG.
 PA (USGO) US GOVERNMENT.
 PA (HEAL-) DEPT. HEALTH & HUMAN SERV.
 PA (USDH) US DEPT HEALTH & HUMAN.
 XX
 PI Crowl RM, Gallo RC, Reddy EP, Shaw GM, Wong-Staal FY;
 XX
 DR WPI: 1986-286067/44.
 DR N-PSDB: AAM60128.
 XX

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XX	PN	W09317705-A.	

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FT Gln at position 392.
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FT Gln at position 397."
FT Misc-difference 406
FT /note= "putative N-linked glycosylation site
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FT His at position 406."
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FT His at position 463."
FT W09317705-A.
FT 16-SEP-1993.
FT 24-FEB-1993: 93WO-US01598.
FT 13-MAR-1992: 92US-0850770.
FT (HARD) HARVARD COLLEGE.
FT Essex ME, Lee C, Lee T, Lee W;
FT MPI: 1993-303140/38.
FT Compos. conty. selectively de-glycosylated HIV-1 envelope protein
FT - shows improved protective immune response
FT Claim 7: Page 15 and 23: 45pp; English.
FT
FT Mutant gp160 env protein C5 is specifically claimed. The
FT amino acid sequence of the mutin does not appear in the
FT specification: sequence R41026 has been derived from the HIV-1 HXB2
FT isolate gp160 env sequence on the SWISS-PROT database (ID = ENV5HIVX,
FT Acc.#: P04578) and the description of C5 mutin given in the
FT specification. The combination of changes made to N-linked
FT glycosylation sites in the C-terminal region of gp120 does not prevent
FT viral infectivity but the resultant selective deglycosylation enables
FT an immune response to be elicited by the mutin.
FT
FT Sequence 856 AA:
SQ
Query Match 96.9%; Score 281; DB 14; Length 856;
Best Local Similarity 96.2%; Pred. No. 1.le-21;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 NHTTWLEMDREINNYTSLHSLIESQNOEKLELLELDKWSLMMNFI 52
DB 624 NHTTWLEMDREINNYTSLHSLIESQNOEKLELLELDKWSLMMNFI 675
RESULT 11
AAR41027
ID AAR41027 standard; protein; 856 AA.
XX
AC AAR41027;
XX
DT 23-MAR-1994 (first entry)
XX
DE Selectively deglycosylated HIV-1 HXB2 env gp160 mutin C6.
XX
XX N-linked glycosylation; gp120: human immunodeficiency virus; type 1;
KM envelope glycoprotein; vaccine; site-directed mutagenesis.
XX
OS Human immunodeficiency virus type 1 (HXB2 strain).
XX
FH Key Location/Qualifiers
FT 1..30
FT Peptide /label= signal_peptide
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FT Protein
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FT /note= "exterior membrane glycoprotein"
FT 512..856
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FT	Gln at position 463"
FN	W09317705-A.
XX	16-SEP-1993.
PD	XX
XX	24-FEB-1993; 93MO-US01598.
PF	XX
PR	13-MAR-1992; 92US-0850770.
XX	XX
PA	(HARD) HARVARD COLLEGE.
XX	XX
PI	Essex ME, Lee C, Lee T, Lee W;
XX	WPI; 1993-303140/38.
DR	XX
XX	Compsn. confg. selectively de-glycosylated HIV-1 envelope protein
PT	- shows improved protective immune response
XX	XX
PS	Claim 7; Page 15 and 23; 45pp; English.
XX	XX
CC	Mutant gp160 env protein C6 is specifically claimed. The
CC	amino acid sequence of the mutein does not appear in the
CC	specification; sequence R41027 has been derived from the
CC	isolate gp160 env sequence on the SWISS-PROT database (ID =
CC	Acc.#: P04578) and the description of C6 mutein given in the
CC	specification. The combination of changes made to N-linked
CC	glycosylation sites in the C-terminal region of gp120 does not prevent
CC	viral infectivity but the resultant selective deglycosylation enables
CC	an immune response to be elicited by the mutein.
XX	Sequence 856 AA;
XX	50

Query Match	96.9%	Score 281;	DB 14;	Length 856;
Best Local Similarity	96.2%	Pred. No. 1.1e-21;		
Matches 50;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;

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Qy 1 NHTTWLEWDREINNTSLIHSLEESONOQOEKLEQELLELDKWSLWNNFNI 52
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Accession	Protein Name	Location/Qualifiers
AA041028	standard; protein; 856 AA.	
AA041028		
AA041028		
23-MAR-1994	(first entry)	
Selectively deglycosylated HIV-1 HXB2 env gp160 mutain Q		
N-linked glycosylation; gp120; human immunodeficiency virus envelope glycoprotein; vaccine; site-directed mutagenesis		
Human immunodeficiency virus type 1 (HXB2 strain).		
Key	Location/Qualifiers	
Peptide	1..30	
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	31..511	
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	/note= "exterior membrane glycoprotein"	
	512..856	
	/label= gp41	
	/note= "transmembrane glycoprotein"	
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FT	eliminated by substitution of Asn by
FT	Gln at position 386"
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FT	His at position 406"
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FT	His at position 463"
PN	WO9317705-A.
XX	16-SEP-1993.
XX	24-FEB-1993; 93WO-US01598.
XX	13-MAR-1992; 92US-0850770.
XX	(HARD) HARVARD COLLEGE.
XX	Essex ME, Lee C, Lee T, Lee W;
XX	WPI; 1993-303140/38.
XX	Compn. contg. selectively de-glycosylated HIV-1 envelope protein
XX	- shows improved protective immune response
XX	Claim 7; Page 18, 23 and 26; 45pp: English.
XX	Mutant gp160 env protein Q is specifically claimed. The
XX	amino acid sequence of the muten does not appear in the

CC	specification: sequence RA1028 has been derived from the HIV-1 HXB2 isolate gp160 env sequence on the SWISS-Prot database (ID = ENVSHYIIX, Acc.# : P0578) and the description of Q protein given in the CC specification. The combination of changes made to N-linked glycosylation sites in the C-terminal region of gp120 does not prevent viral infectivity but the resultant selective deglycosylation enables an immune response to be elicited by the mutain.
XX	
SQ	Sequence 856 AA;
Dy	Query Match 96.9%; Score 281; DB 14; Length 856; Best Local Similarity 96.2%; Pred. No. 1.le-21; Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB	624 1 NHHTWLEMDREINNTSLIHSLIEESONOQEKLDEQLLEDKWMAMMNFNI 52 : : : : : : : : : NHHTWEMDREINNTSLIHSLIEESONOQEKLDELLEDKWMAMMNFNI 675
RESULT 13	
ID	AAR41029
XX	AAR41029 standard; protein; 856 AA.
AC	AAR41029;
DT	23-MAR-1994 (first entry)
XX	Selectively deglycosylated HIV-1 HXB2 env.gp160 mutein R.
DE	
XX	N-linked glycosylation; gp120; human immunodeficiency virus; type 1;
KW	envelope glycoprotein; vaccine; site-directed mutagenesis.
OS	Human immunodeficiency virus type 1 (HXB2 strain).
XX	
FH	Key location/Qualifiers
FT	Peptide 1..30
FT	/label= "signal_peptide"
FT	Protein 31..511
FT	/label= "gp120"
FT	/note= "exterior membrane glycoprotein"
FT	Protein 512..856
FT	/label= "gp41"
FT	/note= "transmembrane glycoprotein"
FT	Modified-site 88
FT	/label= "N-linked_glycosylation_site"
FT	/note= "putative"
FT	Modified-site 136
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FT	/note= "putative"
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FT	/note= "putative"
FT	Modified-site 186
FT	/label= "N-linked_glycosylation_site"
FT	/note= "putative"
FT	Modified-site 197
FT	/label= "N-linked_glycosylation_site"
FT	/note= "putative"
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FT	/note= "putative"
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FT	/label= "N-linked_glycosylation_site"
FT	/note= "putative"
FT	Modified-site 241
FT	/label= "N-linked_glycosylation_site"
FT	/note= "putative"


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FT /note= "putative"
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FT /note= "putative"
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FT Modified-site 448 /label= N-linked glycosylation_site
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FT Modified-site 611 /label= N-linked glycosylation_site
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FT Modified-site 616 /label= N-linked glycosylation_site
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FT Modified-site 674 /label= N-linked glycosylation_site
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FT Modified-site 750 /label= N-linked glycosylation_site
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FT Modified-site 816 /label= N-linked glycosylation_site
FT /note= "putative"
FT Misc-difference 301 /note= "putative"
FT Misc-difference 332 /note= "putative N-linked glycosylation site
FT eliminated by substitution of Asn by
FT His at position 301"
FT Misc-difference 339 /note= "putative N-linked glycosylation site
FT eliminated by substitution of Asn by
FT His at position 332"
FT Misc-difference 386 /note= "putative N-linked glycosylation site
FT eliminated by substitution of Asn by
FT Gln at position 339"

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FT /note= "putative N-linked glycosylation site
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FT Gln at position 386"
FT Misc-difference 397 /note= "putative N-linked glycosylation site
FT eliminated by substitution of Asn by
FT Gln at position 397"
FT Misc-difference 406 /note= "putative N-linked glycosylation site
FT eliminated by substitution of Asn by
FT His at position 406"
FT Misc-difference 463 /note= "putative N-linked glycosylation site
FT eliminated by substitution of Asn by
FT His at position 463"
FT W09317705-A.
FT 16-SEP-1993.
FT 24-FEB-1993; 93WO-US01598.
FT 13-MAR-1992; 92US-0850770.
FT (HARD ) HARVARD COLLEGE.
FT Essex ME, Lee C, Lee T, Lee W;
FT WPI, 1993-303140/38.
FT Compn. conty. selectively de-glycosylated HIV-1 envelope protein
FT - shows improved protective immune response
FT Claim 7: Page 18, 23 and 26; 45pp; English.
FT CC Mutant gp160 env protein S is specifically claimed. The
FT CC amino acid sequence of the muttein does not appear in the
FT CC specification; sequence R41030 has been derived from the HIV-1 HXB2
FT CC isolate gp160 env sequence on the SWISS-PROT database (ID = ENVSHV1X,
FT CC Acc.#: P04578) and the description of S muttein given in the
FT CC specification. The combination of changes made to N-linked
FT CC glycosylation sites in the C-terminal region of gp120 does not prevent
FT CC viral infectivity but the resultant selective deglycosylation enables
FT CC an immune response to be elicited by the muttein.
FT CC
FT SQ Sequence 856 AA:
FT
FT Query Match 96.9%; Score 281; DB 14; Length 856;
FT Best Local Similarity 96.2%; Pred. No. 1.1e-21;
FT Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
FT
FT QY 1 NHTTWMEDREINNTSLIHSLEESONOEKLEOELLEDKWASIMNPNFI 52
FT ID 624 NHTTWMEDREINNTSLIHSLEESONOEKNEOELLEDKWASIMNPNFI 675
FT
FT RESULT 15
FT AAR41031
FT ID AAR41031 standard; protein; 856 AA.
FT AC AAR41031;
FT DT 23-MAR-1994 (first entry)
FT DE Selectively deglycosylated HIV-1 HXB2 env gp160 muttein T.
FT KW N-linked glycosylation; gp120; human immunodeficiency virus; type 1;
FT OS envelope glycoprotein; vaccine; site-directed mutagenesis.
FT FH Human immunodeficiency virus type 1 (HXB2 strain).
FT Key Location/Qualifiers
FT Peptide 1..30

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Wed May 7 14:34:41 2003

Search completed: May 7, 2003, 09:53:57
Job time : 48.4259 secs

us-09-877-606-9.rag

Page 13

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:48:32 ; Search time 17.5741 Seconds
(without alignments)
284.453 Million cell updates/sec

Title: US-09-877-606-9

Perfect score: 290
Sequence: 1 NNTTWLEMDREINNTSLIHSLEESONQOEKLELLEDKWASLMNMFNI 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	268	92.4	851 2 S33985	env polypeptin -
2	268	92.4	854 2 S13288	env polypeptin - huma
3	268	92.4	856 1 VCLJH3	env polypeptin pr
4	268	92.4	861 1 VCLJLV	env polypeptin pr
5	259	89.3	856 1 VCLJLV	env polypeptin pr
6	251	86.6	358 2 S21998	env polypeptin pr
7	245	84.5	856 1 VCLJ3W	env polypeptin pr
8	244	84.1	861 1 VCLJ3C	env polypeptin pr
9	241	83.1	443 2 C41621	env polypeptin p
10	238	82.1	847 2 T09448	env polypeptin p
11	238	82.1	847 2 S13289	env polypeptin - huma
12	236	81.4	852 2 T12016	env polypeptin glycoprot
13	235	81.0	357 2 S21996	env polypeptin g
14	235	81.0	358 2 S22002	env polypeptin g
15	235	81.0	358 2 S22000	env polypeptin g
16	235	81.0	358 2 S70417	env polypeptin g
17	233	80.3	859 1 VCLJMN	env polypeptin g
18	232	80.0	357 2 S22006	env polypeptin pr
19	232	80.0	357 2 S21994	env polypeptin g
20	232	80.0	853 2 S54384	env polypeptin g
21	232	80.0	855 1 VCLJZR	env polypeptin pr
22	231	79.7	357 2 S21992	env polypeptin pr
23	229	79.0	852 1 VCLJBR	env polypeptin g
24	228	78.6	445 2 A41621	env polypeptin -
25	227	78.3	357 2 S22004	env polypeptin M
26	227	78.3	729 1 VCLJRX	env polypeptin g
27	227	78.3	855 1 VCLJAZ	env polypeptin pr
28	227	78.3	861 1 VCLJKB	env polypeptin pr
29	225	77.6	846 1 VCLJND	env polypeptin pr

30	224	77.2	868 1 VCLJH4	env polypeptin -
31	223	76.9	843 1 H44001	env polypeptin pr
32	220	75.9	859 2 J01672	env polypeptin pr
33	219	75.5	136 2 J00266	env polypeptin pr
34	218	75.2	454 2 B41621	env polypeptin p
35	214	73.8	136 2 J00954	env polypeptin p
36	204	70.3	357 2 S21990	env polypeptin g
37	204	70.3	856 1 A44963	env polypeptin g
38	189	65.2	854 1 VCLJST	env polypeptin pr
39	183	63.1	877 2 S49197	env polypeptin pr
40	168	57.9	863 2 A51034	env polypeptin p
41	122	42.1	151 2 S30450	env polypeptin -
42	121	41.7	151 2 S30448	env polypeptin - huma
43	121	41.7	151 2 S30452	env polypeptin - huma
44	121	41.7	151 2 S30451	env polypeptin - huma
45	121	41.7	881 1 VCLJG3	env polypeptin -

ALIGNMENTS

RESULT 1

S33985
env polypeptin - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985
R:Carlini, F.

submitted to the EMBL Data Library, November 1991
A:Reference number: S33979

A:Accession: S33985
A>Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:211530; NID:960192; PIDN:CAA77628.1; PID:960199
C:Superfamily: type E retrovirus env polypeptin

Query Match
Best local similarity 92.4%; Score 268; DB 2; Length 851;
Best local similarity 92.3%; Pred. No. 1.4e-20;

Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNTTWLEMDREINNTSLIHSLEESONQOEKLELLEDKWASLMNMFNI 52
DB 619 NNTTWLEMDREINNTSLIHSLEESONQOEKLELLEDKWASLMNMFNI 670

RESULT 2

S13288
env polypeptin - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

R:O'Brien, W.A.; Koyanagi, Y.; Namasale, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack,
Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp1
A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-854 <COBR>

C:Superfamily: type E retrovirus env polypeptin

Query Match
Best local similarity 92.4%; Score 268; DB 2; Length 854;
Best local similarity 92.3%; Pred. No. 1.4e-20;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NNTTWLEMDREINNTSLIHSLEESONQOEKLELLEDKWASLMNMFNI 52
DB 622 NNTTWLEMDREINNTSLIHSLEESONQOEKLELLEDKWASLMNMFNI 673

RESULT 3

VCLJH3

env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Ratner, L.; Haseltine, W.; Patarca, R.; Liyak, K.J.; Starcich, B.; Josephs, S.F.; Dornberger, J.A.; Papas, T.S.; Ghayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:9326383; PIDN:AAA442
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <SIG>
F:512-856/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 92.4%; Score 268; DB 1; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.4e-20;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTYSLHSLIESQNOEKLEDELDKWSIMMNFNI 52
DB 624 NNTWMEWDREINNTYSLHSLIESQNOEKNEDELDKWSIMMNFNI 675
RESULT 4
VCLJ3W
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LAV-1a)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03975
R:Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Allzon, M.
Cell 40, 9-17, 1985
A:Title: Nucleotide sequence of the AIDS virus, LAV.
A:Reference number: A90866; MUID:8509333; PMID:2981635
A:Accession: A03975
A:Molecule type: DNA
A:Residues: 1-861 <WAI>
A:Cross-references: GB:K02013; NID:9326417; PIDN:AAB59751.1; PID:9326424
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <SIG>
F:512-856/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,402,411
F:616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 92.4%; Score 268; DB 1; Length 861;
Best Local Similarity 92.3%; Pred. No. 1.4e-20;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTYSLHSLIESQNOEKLEDELDKWSIMMNFNI 52
DB 629 NNTWMEWDREINNTYSLHSLIESQNOEKNEDELDKWSIMMNFNI 680
RESULT 5
VCLJ3W
env polypeptide precursor - human immunodeficiency virus type 1 (isolate LV)
N:Alternate names: coat polypeptide

C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03974
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laskey, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retr
A:Reference number: A93353; MUID:85111157; PMID:2982104
A:Accession: A03974
A:Molecule type: DNA
A:Residues: 1-856 <MUS>
A:Cross-references: GB:K02083; NID:9555008; PIDN:AAB59873.1; PID:9328559
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypeptide
F:1-30/Domain: signal sequence #status predicted <SIG>
F:512-856/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 89.3%; Score 259; DB 1; Length 856;
Best Local Similarity 88.5%; Pred. No. 1.3e-19;
Matches 46; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTYSLHSLIESQNOEKLEDELDKWSIMMNFNI 52
DB 624 NNTWMEWDREINNTYSLHSLIESQNOEKNEDELDKWSIMMNFNI 675
RESULT 6
VCLJ3W
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 28
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S21998; S70425
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by
A:Reference number: S21998
A:Accession: S21998
A:Molecule type: DNA
A:Residues: 1-358 <STE>
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70425
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222, 'X', 224-358 <STE2>
A:Cross-references: EMBL:X61359; NID:960182; PIDN:CAA43630.1; PID:960183
C:Superfamily: type E retrovirus env polypeptide
Query Match 86.6%; Score 251; DB 2; Length 358;
Best Local Similarity 84.6%; Pred. No. 3.2e-19;
Matches 44; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNTYSLHSLIESQNOEKLEDELDKWSIMMNFNI 52
DB 126 NNTWMEWDREINNTYSLHSLIESQNOEKNEDELDKWSIMMNFNI 177
RESULT 7
VCLJ3W
env polypeptide precursor - human immunodeficiency virus type 1 (isolate MM1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 07-Nov-1997
C:Accession: A24774

RESULT 12

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T12016
R:McCutchan, F.E.; Sanders-Buell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.
AIDS Res. Hum. Retroviruses 14, 329-337, 1998
A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in
A:Reference number: Z17379; MUID:98178716; PMID:9519894
A:Accession: T12016
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-852 <MC>
A:Cross-References: EMBL:U090934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match 81.4%; Score 236; DB 2; Length 852;
Best Local Similarity 80.8%; Pred. No. 3.6e-17;
Matches 42; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLEESONOQKLEQELLEDKWSLWNNFNI 52
DB 620 DNMTWMEWREIHNTSLIYTLIEESONOQKNEQDLELDKWSLWNNFNI 671

RESULT 13

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-References: EMBL:X61356; NID:g60181; PIDN:CAA43624.1; PID:g1067129
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match 81.0%; Score 235; DB 2; Length 357;
Best Local Similarity 78.8%; Pred. No. 1.6e-17;
Matches 41; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLEESONOQKLEQELLEDKWSLWNNFNI 52
DB 125 DNMTWMEWREIHNTSLIYTLIEESONOQKNEQDLELDKWSLWNNFNI 176

RESULT 14

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 3L
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 01-Dec-2000
C:Accession: S22002; S70418
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determi
A:Reference number: S21990
A:Accession: S22002
A:Molecule type: DNA
A:Residues: 1-358 <STEL>
A:Cross-References: EMBL:X61352; NID:g60186; PIDN:CAA43616.1; PID:g60187
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cer
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333, 'X', 335-358 <STEL>
A:Cross-References: EMBL:X61352; NID:g60186
C:Superfamily: type E retrovirus env polyprotein

Query Match 81.0%; Score 235; DB 2; Length 358;
Best Local Similarity 78.8%; Pred. No. 1.6e-17;
Matches 41; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLEESONOQKLEQELLEDKWSLWNNFNI 52
DB 126 DNMTWMEWREIHNTSLIYTLIEESONOQKNEQDLELDKWSLWNNFNI 177

RESULT 15

envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 12-Apr-1995
C:Accession: S22000
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as dete
A:Reference number: S21990
A:Accession: S22000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <STEL>
A:Cross-References: EMBL:X61351
C:Superfamily: type E retrovirus env polyprotein

Query Match 81.0%; Score 235; DB 2; Length 358;
Best Local Similarity 78.8%; Pred. No. 1.6e-17;
Matches 41; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTSLIHSLEESONOQKLEQELLEDKWSLWNNFNI 52
DB 126 DNMTWMEWREIHNTSLIYTLIEESONOQKNEQDLELDKWSLWNNFNI 177

Search completed: May 7, 2003, 09:58:43
Job time: 18.5741 secs

FT DISULFID 385 418 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;

Query Match Best Similarity 96.9%; Score 281; DB 1; Length 856;
 Best Local Similarity 96.2%; Pred. No. 1.5e-22;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLMDREINNTSLHSIESQNOEKLEDELDKWSLMMNFI 52
 DB 624 NHTTWLMDREINNTSLHSIESQNOEKLEDELDKWSLMMNFI 675

RESULT 2
 ID ENV_HV1H3 STANDARD; PRT; 856 AA.
 AC P04624;
 DT 13-AUG-1987 (rel. 05, Created)
 DT 01-FEB-1996 (rel. 33, Last annotation update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11707;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85228248; PubMed=2988795;
 RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;
 RT "HIV-1 env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";
 RL Cell 41:979-986(1985).
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 CC -----

DR EMBL: M14100; AAA44679.1; -
 DR HIV; M14100; ENVSHXB3.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 DR Aids; Coat protein; Polypeptide; glycoprotein; Transmembrane; signal.

FT SIGNAL 1 30
 FT CHAIN 1 511
 FT CHAIN 512 856
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

Query Match Best Similarity 96.9%; Score 281; DB 1; Length 856;
 Best Local Similarity 96.2%; Pred. No. 1.5e-22;
 Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLMDREINNTSLHSIESQNOEKLEDELDKWSLMMNFI 52
 DB 624 NHTTWLMDREINNTSLHSIESQNOEKLEDELDKWSLMMNFI 675

RESULT 3
 ID ENV_HV1LW STANDARD; PRT; 856 AA.
 AC Q70626;
 DT 15-JUL-1998 (rel. 36, Created)
 DT 15-JUL-1998 (rel. 36, Last annotation update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (LM12.3 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 CC -----

[illegible]

OY	1	HTTLELNDREINNTSLHSLSIESONOELEBELLFLDKNASLNWNTI	52
D6	624	NHTTWEMDREINNTSLHSLSIESONOEKNEQELLELDKWASLMWNFI	675

RESULT 4

ENV_HV1B8

ID

ENV_HV1B8

STANDARD:

PRT:

851 AA.

AC

P04582:

DT

13-AUG-1987

(Rel. 05, Created)

DT

13-AUG-1987

(Rel. 05, Last sequence update)

DT

15-JUL-1999

(Rel. 38, Last annotation update)

DE

Envelope polypeptide gp160 precursor [contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

CN

ENV.

OS

Human immunodeficiency virus type 1 (BH8 isolate) (HIV-1).

OC

Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX

NCBI_TaxID=11684;

RN

[1]

RP

SEQUENCE FROM N.A.

RX

MEDLINE=8511123; PubMed=2578615;

RA

Katner L., Haseltine W., Patarca R., Liyak K.J., Starcich B.R., Josephs S.F., Doran E.R., Ratsiski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Peteway S.R. Jr., Pearson M.D., LaTenberger J.A., Pappas T.S., Graybe J., Chang N.T., Gallo R.C., Wong-Staal F.;

RA

"Complete nucleotide sequence of the AIDS virus, HTLV-III.";

RL

Nature 313:277-284(1985).

CC

CC

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CC

DR

EMBL; K02011; AAAA44661.1; "-

DR

HIV; K02011; ENVGBH8.

DR

GlycosultedB; P04582; "-

DR

InterPro: IPR000328; Env.GP41.

DR

InterPro: IPR000777; GP120.

DR

Pfam; PF00516; GP120; 1.

KW

Pfam; PF00516; GP41; 1.

DR

AIDS; Coat protein; Glycoprotein; Transmembrane; Signal.

KW

SIGNAL.

FT

SIGNAL

1 30

EXTERIOR MEMBRANE GLYCOPROTEIN.

FT

CHAIN

31 506

TRANSMEMBRANE GLYCOPROTEIN.

FT

CHAIN

507 851

BY SIMILARITY.

FT

DISULFID

54 74

BY SIMILARITY.

FT

DISULFID

119 205

BY SIMILARITY.

FT

DISULFID

126 196

BY SIMILARITY.

FT

DISULFID

131 157

BY SIMILARITY.

FT

DISULFID

218 247

BY SIMILARITY.

FT

DISULFID

228 239

BY SIMILARITY.

FT

DISULFID

296 331

BY SIMILARITY.

FT

DISULFID

378 440

BY SIMILARITY.

FT

DISULFID

385 413

BY SIMILARITY.

FT

CARBOHYD

88 88

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

136 136

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

141 141

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

156 156

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

160 160

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

186 186

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

197 197

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

230 230

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

234 234

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

241 241

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

262 262

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

276 276

N-LINKED (GLCNAC . .) (POTENTIAL).

FT

CARBOHYD

295 295

N-LINKED (GLCNAC . .) (POTENTIAL).

FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;

Query Match Score 268; DB 1; Length 851;
 Best Local Similarity 92.3%; Pred. No. 3.7e-21;
 Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTWTLEMDREINNTSLHSLIESONOKEKLEDELDKWSLMMNFI 52
 DB 619 NHTWTLEMDREINNTSLHSLIESONOKEKLEDELDKWSLMMNFI 670

RESULT 5
 ENV_HV1B1 STANDARD; PRT; 856 AA.

AC P03375;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BHI isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11678;
 RX MEDLINE=8511123; PubMed=2578615;
 RA Rafter L., Haseltine W., Patarca R., Liyak K.J., Starcich B.R., Josephs S.F., Doran E.R., Ratslaski J.A., Whitehorn E.A., Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L., Lautenberger J.A., Pappas T.S., Chrayeb J., Chang N.T., Gallo R.C., Wong-Staal F.;
 RA Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RA Nature 313:277-284(1985).
 RN [2]
 RP DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=90285159; PubMed=2355006;
 RA Leonard C.K., Spellman M.W., Riddle L., Harris R.J., Thomas J.N., Gregory T.J.;
 RA "Assignment of intrachain disulfide bonds and characterization of potential glycosylation sites of the type I recombinant human immunodeficiency virus envelope glycoprotein (GP120) expressed in Chinese hamster ovary cells.";
 RA J. Biol. Chem. 265:10373-10382(1990).
 CC -----
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 CC -----
 CC EMBL: M15654; AAA44205.1;
 DR PIR: A03973; VCIJH3.
 DR HIV: M15654; ENVSRH102.
 DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP41; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Glycoprotein; Polypeptide; Transmembrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 511
 FT CHAIN 512 856
 FT DISULFID 54 74
 FT DISULFID 119 205
 FT DISULFID 126 196
 FT DISULFID 131 157
 FT DISULFID 218 247
 FT DISULFID 228 239
 FT DISULFID 296 331
 FT DISULFID 378 445
 FT DISULFID 385 418
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 230 230 N-LINKED (GLCNAC. . .)
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 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .)
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 FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. . .)
 FT CARBOHYD 611 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 674 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 750 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 816 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 856 AA; 97224 MW; 0BFB1A18931B827 CRC64;

Query Match Score 268; DB 1; Length 856;
 Best Local Similarity 92.3%; Pred. No. 3.7e-21;
 Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTWTLEMDREINNTSLHSLIESONOKEKLEDELDKWSLMMNFI 52
 DB 624 NHTWTLEMDREINNTSLHSLIESONOKEKLEDELDKWSLMMNFI 675

RESULT 6
 ENV_HV1B1 STANDARD; PRT; 861 AA.

AC P03377;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11686;
 RN [1]

Query Match	Best Local Similarity	Score 265;	DB 1;	Length 853;
Matches 47;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	1	1	1
Db	622	NNMTWEMREINNTYSLIHSLIHESONOEKLEDELMDKASLMMNFI	52	673
RESULT 8				
ENV_HV1PV	ENV_HV1PV	STANDARD:	PRT:	856 AA.
AC	P03376;			
DT	21-JUL-1986 (Rel. 01, created)			
DT	21-JUL-1986 (Rel. 01, last sequence update)			
DT	15-JUL-1999 (Rel. 38, last annotation update)			
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_Taxid:11700;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=8511157; Pubmed=2982104;			
RA	Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A., Capon D.J.;			
RT	"Nucleic acid structure and expression of the human AIDS/Lymphadenopathy retrovirus.";			
RL	Nature 313:450-458(1985).			
CC	-----			
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CC	-----			
DR	EMBL; K02083; AAB59873.1; .			
DR	EMBL; X01762; CAA25903.1; ALT_SEQ.			
DR	PIR; A03974; VCLJVL.			
DR	HIV; K02083; ENVSPV22.			
DR	InterPro; IPR000328; ENV_GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.			
FT	SIGNAL	1	30	
FT	CHAIN	31	511	
FT	CHAIN	512	856	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	157	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.

FT	DISTLFTD	296	331		BY SIMILARITY.
FT	DISTLFTD	378	445		BY SIMILARITY.
FT	DISTLFTD	385	418		BY SIMILARITY.
FT	CARBOHYD	88		N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	136	136	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	141	141	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	156	156	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	186	186	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	197	197	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	230	230	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	234	234	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	241	241	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	262	262	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	276	276	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	289	289	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	295	295	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	301	301	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	339	339	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	356	356	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	386	386	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	392	392	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	397	397	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	448	448	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	463	463	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	611	611	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	616	616	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	625	625	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	637	637	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	674	674	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	750	750	N-LINKED (GLCNAC . .)	(POTENTIAL).
FT	CARBOHYD	816	816	N-LINKED (GLCNAC . .)	(POTENTIAL).
SO	SEQUENCE	856 AA:	97339 MW;	5FCDBIDJC3C1209B3 CXC64;	
	Query Match	Best Local Similarity	89.3%;	Score 259; DB 1; Length 856;	
	Matches	46; Conservative	3; Mismatches	3; Indels	0; Gaps
OY	1 NHTTLEMDREINNTYTSLHSHIESQNOQEDELDELDWASLMMFN1	52			
Db	624 NNMTGMEWDREINNTYTSLHSHIESQNOQEDELDELDWAMLMNMLNI	675			
RESULT 9					
ID	ENV_HV1M1	STANDARD:	PRT:	856 AA.	
AC	P31872:				
DT	01-JUL-1993 (Rel. 26, Created)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].				
OS	ENV.				
OS	Human immunodeficiency virus type 1 (WMJ1 isolate) (HIV-1).				
OC	Viruses; Retroid viruses; Retroviridae; Lentivirns.				
OX	NCBI_TaxID=31678;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=86218077; PubMed=2423250;				
RA	Starck B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.; "Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";				
RL	Cell 45:637-648(1986).				
CC	-I- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SPONTANEOUSLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.				
CC	PIR: A24774; VCL33W.				
OR	InterPro: IPR000328; Env_GP41.				
OR	InterPro: IPR000777; GP120.				

Query Match	Best Local Similarity	Score	DB 1:	Length
Matches 43; Conservative 7; Mismatches 2; Indels 0; Gaps 0	84.5%;	245;	DB1:	856;
			Pred. No. 1.e-18;	
OY 1	1	1	1	1
Db 624	624	624	624	624
ENV_HV1SC	ENV_HV1SC	ENV_HV1SC	ENV_HV1SC	ENV_HV1SC
STANDARD:	STANDARD:	STANDARD:	STANDARD:	STANDARD:
PRT:	PRT:	PRT:	PRT:	PRT:
856 AA.	856 AA.	856 AA.	856 AA.	856 AA.
AC P05878;	AC P05878;	AC P05878;	AC P05878;	AC P05878;
DT 01-NOV-1988 (Rel. 09, Created)	DT 01-NOV-1988 (Rel. 09, Created)	DT 01-NOV-1988 (Rel. 09, Created)	DT 01-NOV-1988 (Rel. 09, Created)	DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)	DT 01-NOV-1988 (Rel. 09, Last sequence update)	DT 01-NOV-1988 (Rel. 09, Last sequence update)	DT 01-NOV-1988 (Rel. 09, Last sequence update)	DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)	DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).	DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).	DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).	DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).	DE Envelope glycoprotein (GP120); Transmembrane glycoprotein (GP41).
GN ENV.	GN ENV.	GN ENV.	GN ENV.	GN ENV.
OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).	OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).	OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).	OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).	OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
OC Viruses: Retroid viruses; Retroviridae; Lentivirus.	OC Viruses: Retroid viruses; Retroviridae; Lentivirus.	OC Viruses: Retroid viruses; Retroviridae; Lentivirus.	OC Viruses: Retroid viruses; Retroviridae; Lentivirus.	OC Viruses: Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11702;	OX NCBI_TaxID=11702;	OX NCBI_TaxID=11702;	OX NCBI_TaxID=11702;	OX NCBI_TaxID=11702;
RP [1]	RP [1]	RP [1]	RP [1]	RP [1]
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;	RX MEDLINE=88219542; PubMed=3369091;	RX MEDLINE=88219542; PubMed=3369091;	RX MEDLINE=88219542; PubMed=3369091;	RX MEDLINE=88219542; PubMed=3369091;
RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,	RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,	RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,	RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,	RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.	RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.	RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.	RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.	RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S., Jr.
RT "Envelope sequences of two new United States HIV-1 isolates."	RT "Envelope sequences of two new United States HIV-1 isolates."	RT "Envelope sequences of two new United States HIV-1 isolates."	RT "Envelope sequences of two new United States HIV-1 isolates."	RT "Envelope sequences of two new United States HIV-1 isolates."
RL VIROLOGY 164:531-536(1988).	RL VIROLOGY 164:531-536(1988).	RL VIROLOGY 164:531-536(1988).	RL VIROLOGY 164:531-536(1988).	RL VIROLOGY 164:531-536(1988).

```
CC -1- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN  
CC 1984 IN SOUTHERN CALIFORNIA.  
-----  
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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CC modified and this statement is not removed. Usage by and for commercial  
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CC or send an email to license@isb.ch).  
-----  
DR EMBL: M17450; -: NOT_ANNOTATED_CDS.  
DR PIR: B28922; VCLJSC.  
DR HIV: M17450; ENVSSC.  
DR InterPro: IPRO00328; Env-GP41.  
DR Pfam: PF00516; GP120; 1.  
DR pfam: PF00517; GP41; 1.  
KW AIDS; Coat protein; Glycoprotein; Polypotein; Transmembrane;  
KW Signal.  
FT SIGNAL 1 29  
FT CHAIN 30 510 EXTERIOR MEMBRANE GLYCOPROTEIN.  
FT CHAIN 511 856 TRANSMEMBRANE GLYCOPROTEIN.  
FT SITE 760 760 IN-FRAME TERMINATION CODON.  
FT DISULFID 53 73 BY SIMILARITY.  
FT DISULFID 118 206 BY SIMILARITY.  
FT DISULFID 125 197 BY SIMILARITY.  
FT DISULFID 130 160 BY SIMILARITY.  
FT DISULFID 219 247 BY SIMILARITY.  
FT DISULFID 228 239 BY SIMILARITY.  
FT DISULFID 296 330 BY SIMILARITY.  
FT DISULFID 376 439 BY SIMILARITY.  
FT DISULFID 383 412 BY SIMILARITY.  
FT CARBOHYD 87 87 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 129 129 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 135 135 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 140 140 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 143 143 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 159 159 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 163 163 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 189 189 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 198 198 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 234 234 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 241 241 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 262 262 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 276 276 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 295 295 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 301 301 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 302 302 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 331 331 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 338 338 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 354 354 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 360 360 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 384 384 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 394 394 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 400 400 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 405 405 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 442 442 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 457 457 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 611 611 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 616 616 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 625 625 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 637 637 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 674 674 N-LINKED (GLCNAC . .) (POTENTIAL).  
FT CARBOHYD 816 816 N-LINKED (GLCNAC . .) (POTENTIAL).  
SO SEQUENCE 856 AA; 97055 MW; DAF4DA600EBA7A08 CRC64;  
  
Query Match 84.1%; Score 244; DB 1; Length 856;  
Best Local Similarity 87.8%; Pred. No. 1.4e-18;  
Matches 43; Conservative 5; Mismatches 1; Indels 0; Gaps 0.
```

DB 627 TWMEWEIDNTSLVTLIESONOEKNEQELLEDKWSLMMNFSI 675

RESULT 11

ENV_HV1S1

ENV_HV1S3 STANDARD; PRT; 852 AA.

AC P19549; 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11690;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90317906; PubMed=2370688;

RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;

RT *Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.*

RT J. Virol. 64:4016-4020(1990).

RL -----

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CC -----

CC EMBL: M38427; AAA45067.1; -

DR HIV: M38427; ENVSEF33.

DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 31 BY SIMILARITY.

FT CHAIN 506 852 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 118 206 BY SIMILARITY.

FT DISULFID 125 197 BY SIMILARITY.

FT DISULFID 130 156 BY SIMILARITY.

FT DISULFID 219 248 BY SIMILARITY.

FT DISULFID 229 240 BY SIMILARITY.

FT DISULFID 257 331 BY SIMILARITY.

FT DISULFID 377 439 BY SIMILARITY.

FT DISULFID 384 412 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL).

SO SEQUENCE 852 AA; 96663 MW; EF7BBFED23C9910D CRC64;

Query Match 83.8%; Score 243; DB 1; Length 852;

Best Local Similarity 80.8%; Pred. No. 1.7e-18;

Matches 42; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

DB 620 NNMTWMEWEIDNTSLVTLIESONOEKNEQELLEDKWSLMMNFSI 671

QY 1 NHTTWLEMEWEIDNTSLVTLIESONOEKNEQELLEDKWSLMMNFSI 52

RESULT 12

ENV_HV1S1

ENV_HV1S1 STANDARD; PRT; 847 AA.

AC P19550; 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Envelope polypeptide gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN ENV.

OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).

OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11691;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90347835; PubMed=2384920;

RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;

RT *Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.*

RT J. Virol. 64:4390-4398(1990).

RL -----

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CC -----

CC EMBL: M65024; AAA45072.1; -

DR HIV: M38428; ENVSEF162.

DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00517; GP120; 1.

DR Pfam: PF00517; GP41; 1.

KW Aids; Coat protein; Glycoprotein; Transmembrane; Signal.

KW SIGNAL.

FT CHAIN 1 29 EXTERIOR MEMBRANE GLYCOPROTEIN.

FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.

FT DISULFID 53 73 BY SIMILARITY.

FT DISULFID 118 203 BY SIMILARITY.

FT DISULFID 125 194 BY SIMILARITY.

FT DISULFID 130 155 BY SIMILARITY.

FT DISULFID 216 245 BY SIMILARITY.

FT DISULFID 226 237 BY SIMILARITY.

FT DISULFID 294 328 BY SIMILARITY.

FT DISULFID 374 435 BY SIMILARITY.

FT DISULFID 381 408 BY SIMILARITY.

FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).

50	SEQUENCE	847 AA;	96135 MM;	0A901317ED7F72AB	CR664;
FT	CARBOHYD	195	195	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	232	232	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	239	239	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	260	260	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	274	274	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	299	299	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	329	329	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	336	336	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	352	352	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	382	382	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	388	388	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	392	392	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	398	398	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	401	401	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	438	438	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	454	454	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	602	602	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. . .)	(POTENTIAL)
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. . .)	(POTENTIAL)

Query Match	83.4%	Score 242;	DB 1;	Length 847;
Best Local Similarity	80.8%	Pred. No. 2.2e-18;		
Matches 42; Conservative	8;	Mismatches 2;	Indels 0;	Gaps

[illegible]

RESULT 13	
ENV_HV1W2	
ID ENV_HV1W2	STANDARD;
	PRT; 847 AA

DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
CN ENV.

OS Human immunodeficiency virus type 1 (WMJ2 isolate)
OC Viruses; Retrovid viruses; Retroviridae; Lentivirus
OX NCBI_TaxID=11705;

RN [1]
RP SEQUENCE FROM N.A.
DR

RX MEDLINE=86235450; PubMed=30127178;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
Cobarrubias A.G., et al. (1991) The

RT "Genetic variation in HIV-III/LAV over time in patients with AIDS and at risk for AIDS".

CC	-1-	MISCELLANEOUS; ISOLATES	EMT1	EMT2	AND EM
RL	Science	232:1548-1553(1986).			
NI	ALLISK	FOR AIDS.			

1. MISCELLANEOUS ISOLATES WIND 1, WIND 2, AND WIND 3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER

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```
CC -----
DR EMBL; M12507; AAB12990.1; -.
```

DR HIV; M12507; ENV\$MMJ2.
DR InterPro; IPR000328; Env_GP41

DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR ProSITE; PS00511; GP120; 1.

DR PIAM; PF005117; GPAL; 1.
KW AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane protein

am
stigmaL.

FT	SIGNAL	1	29	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	30	501	TRANSMEMBRAN GLYCOPROTEIN.
FT	CHAIN	502	847	
FT	DISULFID	53	73	BY SIMILARITY.
FT	DISULFID	118	202	BY SIMILARITY.
FT	DISULFID	125	193	BY SIMILARITY.
FT	DISULFID	130	152	BY SIMILARITY.
FT	DISULFID	215	244	BY SIMILARITY.
FT	DISULFID	225	236	BY SIMILARITY.
FT	DISULFID	293	326	BY SIMILARITY.
FT	DISULFID	372	435	BY SIMILARITY.
FT	DISULFID	379	408	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	134	134	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	140	140	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	194	194	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	231	231	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	238	238	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	259	259	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	273	273	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	286	286	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	327	327	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	334	334	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	350	350	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	356	356	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	380	380	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	386	386	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	438	438	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	602	602	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	607	607	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	616	616	N-LINKED (GLCNAC. .) (POTENTIAL)
FT	CARBOHYD	628	628	N-LINKED (GLCNAC. .) (POTENTIAL)
50	SEQUENCE	847 AA:	96466 MW:	CD133D73AA5B0AC CR664:

Query Match %:	80.7%	Score 234;	DB 1;	Length 847;
Best Local Similarity:	78.8%	Pred. No. 1.6e-17;		
Matches 41;	Conservative	8;	Mismatches 3;	Indels 0;
			Gaps	0

[illegible]

RESULT 14	
ENV_HV1MN	STANDARD;
ID ENV_HV1MN	PRT; 856 AA

AC	P05877;
DT	01-NOV-1988 (Rel. 09, Created)

DT	01-NOV-1988 (Rel. 09, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)

DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

GN
ENV,
OS
Human immunodeficiency virus type 1 (MN isolate) (HIV-1)
OC
Viruses: Botryoid viruses; Botryoid virus; Botryoid virus

CC	viruses; reoviridae; reovirus.
OC	
RN	NCBI_TaxID=11696;
	[1]

SEQUENCE FROM N.A.
MEDLINE-882195423

RA Gurgo C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.:

RT "Envelope sequences of two new United States HIV-1 isolates."
RL Virology 164:531-536(1988).

CC -I- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC

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DR EMBL: M17449; AAA44857.1; -
 DR PIR: A28922; VCLJMN.
 DR HIV: M17449; ENVSMN.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.

FT SIGNAL. 1 29
 FT CHAIN 30 513
 FT CHAIN 514 856
 FT DISULFID 53 73
 FT DISULFID 118 210
 FT DISULFID 125 201
 FT DISULFID 130 162
 FT DISULFID 223 252
 FT DISULFID 233 244
 FT DISULFID 301 335
 FT DISULFID 381 445
 FT DISULFID 388 418
 FT DISULFID 87 87
 FT CARBOHYD 129 129
 FT CARBOHYD 135 135
 FT CARBOHYD 140 140
 FT CARBOHYD 141 141
 FT CARBOHYD 146 146
 FT CARBOHYD 161 161
 FT CARBOHYD 165 165
 FT CARBOHYD 191 191
 FT CARBOHYD 202 202
 FT CARBOHYD 246 246
 FT CARBOHYD 267 267
 FT CARBOHYD 281 281
 FT CARBOHYD 294 294
 FT CARBOHYD 300 300
 FT CARBOHYD 336 336
 FT CARBOHYD 343 343
 FT CARBOHYD 359 359
 FT CARBOHYD 365 365
 FT CARBOHYD 395 395
 FT CARBOHYD 401 401
 FT CARBOHYD 405 405
 FT CARBOHYD 406 406
 FT CARBOHYD 413 413
 FT CARBOHYD 448 448
 FT CARBOHYD 465 465
 FT CARBOHYD 612 612
 FT CARBOHYD 617 617
 FT CARBOHYD 626 626
 FT CARBOHYD 638 638
 FT CARBOHYD 816 816
 SQ SEQUENCE 856 AA; 97140 MW; D197DB09940BE732 CRC64;

Query Match 80.3%; Score 233; DB 1; Length 856;
 Best Local Similarity 76.9%; Pred. No. 2e-17;
 Matches 40; Conservative 9; Mismatches 3; Indels 0; Gaps 0;

OY 1 NHTTLEMBREINNTYSLHSLEESONQOEKLEFLLDLDMWASIMNPNFI 52
 DB 625 NNNNTMOMEREIDNNTSLIYSLEKSOEQOEKNEDELLDMWASIMNPNFI 676

RESULT 15

ENV_HV122
 ID ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.

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DR EMBL: M22639; AAA45370.1; -
 DR HIV: M22639; ENV8226.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.

FT SIGNAL. 1 31
 FT CHAIN 32 508
 FT CHAIN 509 853
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 154
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 330
 FT DISULFID 376 442
 FT DISULFID 383 415
 FT DISULFID 87 87
 FT CARBOHYD 137 137
 FT CARBOHYD 144 144
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 185 185
 FT CARBOHYD 188 188
 FT CARBOHYD 198 198
 FT CARBOHYD 235 235
 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
 FT CARBOHYD 277 277
 FT CARBOHYD 290 290
 FT CARBOHYD 296 296
 FT CARBOHYD 331 331
 FT CARBOHYD 338 338
 FT CARBOHYD 353 353
 FT CARBOHYD 384 384
 FT CARBOHYD 390 390
 FT CARBOHYD 402 402
 FT CARBOHYD 441 441
 FT CARBOHYD 445 445
 FT CARBOHYD 458 458
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 FT CARBOHYD 608 608
 FT CARBOHYD 613 613
 FT CARBOHYD 622 622

ENV_HV122
 ID ENV_HV122 STANDARD; PRT; 853 AA.
 AC P12487;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
 GN ENV.
 OS Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11683;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Theodore T., Buckler-White A.;
 RL Submitted (NOV-1988) to the HIV data bank.

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DR EMBL: M22639; AAA45370.1; -
 DR HIV: M22639; ENV8226.
 DR InterPro: IPR000328; Env GP41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW Aids; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
 KW Signal.

FT SIGNAL. 1 31
 FT CHAIN 32 508
 FT CHAIN 509 853
 FT DISULFID 53 73
 FT DISULFID 118 206
 FT DISULFID 125 197
 FT DISULFID 130 154
 FT DISULFID 219 248
 FT DISULFID 229 240
 FT DISULFID 297 330
 FT DISULFID 376 442
 FT DISULFID 383 415
 FT DISULFID 87 87
 FT CARBOHYD 137 137
 FT CARBOHYD 144 144
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 FT CARBOHYD 157 157
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 FT CARBOHYD 188 188
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 FT CARBOHYD 242 242
 FT CARBOHYD 263 263
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 FT CARBOHYD 290 290
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 FT CARBOHYD 331 331
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 FT CARBOHYD 613 613
 FT CARBOHYD 622 622

Wed May 7 14:34:43 2003

us-09-877-606-9.rsp

Page 11

FT	CARBOHYD	634	634	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	671	671	N-LINKED (GLCNAC. . .)	(POTENTIAL).
SQ	SEQUENCE	853 AA;	97043 MW;	849B08CBAFF7008	CRC64;

Query Match	80.0%;	Score 232;	DB 1;	Length 853;
Best Local Similarity	83.7%;	Pred. No. 2.6e-17;		
Matches 41;	Conservative 4;	Mismatches 4;	Indels 0;	Gaps 0;

OY 4 TWLEMDREINNYTSLIHSIIESQNOOEKLEQLLELTDKWSLWNFNI 52
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 624 TWMWEERIDNNTGLIYLRIIESQTQOEKNQEELLELDKWSLWNFNI 672

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Search completed: May 7, 2003, 09:54:41
Job time : 10.1481 secs
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2003, 09:47:22 ; Search time 37.3148 Seconds

(without alignments)
287.137 Million cell updates/sec

Title: US-09-877-606-9

Perfect score: 290
Sequence: 1 NHRTWLEMDREINNTSLH.....LEQELLELDKWSLWMTFNI 52

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPRTEMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_minc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	281	96.9	748	15	Q70606 human immun
2	281	96.9	752	15	Q70604 human immun
3	281	96.9	752	15	Q70605 human immun
4	277	95.5	747	15	Q70607 human immun
5	277	95.5	752	15	Q70608 human immun
6	276	95.2	856	15	Q905M7 human immun
7	273	94.1	852	15	Q89797 human immun
8	270	93.1	856	15	Q92877 simian-huma
9	268	92.4	645	15	Q993A6 human immun
10	268	92.4	851	15	Q78243 human immun
11	268	92.4	854	15	Q85582 human immun
12	268	92.4	854	15	Q72502 human immun
13	268	92.4	856	15	Q74599 human immun
14	264	91.0	854	15	Q74090 human immun
15	264	91.0	854	15	Q90178 human immun
16	264	91.0	854	15	Q78705 human immun

17	257	88.6	757	15	Q9Q722 human immun
18	256	88.3	855	15	Q9E1R7 human immun
19	255	87.9	848	15	Q69990 human immun
20	254	87.6	851	15	Q56110 human immun
21	253	87.2	727	15	Q9Q723 human immun
22	252	86.9	616	15	Q993B0 human immun
23	252	86.9	618	15	Q993B2 human immun
24	251	86.6	358	15	Q78120 human immun
25	251	86.6	848	15	Q69988 human immun
26	250	86.2	635	15	Q90082 human immun
27	250	86.2	838	15	Q03806 human immun
28	250	86.2	852	15	Q69992 human immun
29	250	86.2	854	15	Q78225 human immun
30	250	86.2	855	15	Q03805 human immun
31	249	85.9	862	15	Q9E1S2 human immun
32	248	85.5	856	15	Q72993 human immun
33	248	85.5	859	15	Q80863 human immun
34	247	85.2	851	15	Q80852 human immun
35	247	85.2	863	15	Q9W0U4 human immun
36	247	85.2	864	15	Q9W0U4 human immun
37	246	84.8	847	15	Q69996 human immun
38	246	84.8	854	15	Q56112 human immun
39	246	84.8	863	15	Q9W0U8 human immun
40	246	84.8	863	15	Q42031 human immun
41	246	84.8	864	15	Q9W0U1 human immun
42	245	84.5	849	15	Q77368 human immun
43	244	84.1	684	15	Q91K06 human immun
44	244	84.1	847	15	Q41537 human immun
45	244	84.1	855	15	Q91K00 human immun

ALIGNMENTS

RESULT 1

ID Q70606 PRELIMINARY; PRT; 748 AA.
AC Q70606;
DT 01-NOV-1996 (TRENBERG, 01, Created)
DI 01-NOV-1996 (TRENBERG, 01, Last sequence update)
DT 01-DEC-2001 (TRENBERG, 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.,
"Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HIV type IIIB)."
RT AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LM881;
RA Mulder K.E.;
DR Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12032; AAA/6668.1; -;
DR InterPro: IPR000328; Env_GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT
FT NON_TER
SQ
SEQUENCE 748 AA; 84224 MW; 56BBDP186C67694B CRC64;

Query Match 96.9%; Score 281; DB 15; Length 748;
Best Local Similarity 96.2%; Pred. No. 6.6e-21;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 NHTTLEMDREINNTSLIHSLEESQNOEKLEQELLELDKWSLMMNFI 52
DB 620 NHTTWMEDREINNTSLIHSLEESQNOEKNEQELLELDKWSLMMNFI 671

RESULT 2
OY 070604 PRELIMINARY; PRT; 752 AA.
AC 070604;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RX MEDLINE=95127297; PubMed=7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Vital variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIIB).";
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM851;
RA Mulder K.E.;
RN Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12030; AAA7666.1; -
DR InterPro: IPR000328; Env-GP41.
DR Pfam: PF00516; GP120. 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 281; DB 15; Length 752;
Best Local Similarity 96.2%; Pred. No. 6.7e-21;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLIHSLEESQNOEKLEQELLELDKWSLMMNFI 52
DB 624 NHTTWMEDREINNTSLIHSLEESQNOEKNEQELLELDKWSLMMNFI 675

RESULT 3
OY 070605 PRELIMINARY; PRT; 752 AA.
AC 070605;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM852;
RX MEDLINE=95127297; PubMed=7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Vital variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIIB).";
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM852;

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RA Mulder K.E.;
RN Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12031; AAA7667.1; -
DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 752
SQ SEQUENCE 752 AA; 84894 MW; 8B30AE894013B45A CRC64;

Query Match 96.9%; Score 281; DB 15; Length 752;
Best Local Similarity 96.2%; Pred. No. 6.7e-21;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLIHSLEESQNOEKLEQELLELDKWSLMMNFI 52
DB 624 NHTTWMEDREINNTSLIHSLEESQNOEKNEQELLELDKWSLMMNFI 675

RESULT 4
OY 070607 PRELIMINARY; PRT; 747 AA.
AC 070607;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RX MEDLINE=95127297; PubMed=7826699;
RA Reltz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
RT "Vital variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIIB).";
RN AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-LM87-1;
RA Mulder K.E.;
RN Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
DR EMBL: U12034; AAA7666.1; -
DR InterPro: IPR000328; Env-GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120. 1.
DR AIDS; Coat protein; Glycoprotein; Polyprotein; Transmembrane.
FT NON_TER 747
SQ SEQUENCE 747 AA; 84250 MW; 732E836A52245F14 CRC64;

Query Match 95.5%; Score 277; DB 15; Length 747;
Best Local Similarity 96.2%; Pred. No. 1.7e-20;
Matches 50; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTLEMDREINNTSLIHSLEESQNOEKLEQELLELDKWSLMMNFI 52
DB 619 NHTTWMEDREINNTSLIHSLEESQNOEKNEQELLELDKWSLMMNFI 670

RESULT 5
OY 070608 PRELIMINARY; PRT; 752 AA.
AC 070608;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DE Envelope glycoprotein (Fragment).
GN ENV.

```

OS Human immunodeficiency virus type 1
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM87-2;
 RX MEDLINE=95127297; PubMed=7826699.
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM87-2;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12035; AAA76671.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 FT NON_TER 752
 SQ SEQUENCE 752 AA; 84780 MW; 708672A2D0C0E8F8 CRC64;

Query Match 95.5%; Score 277; DB 15; Length 752;
 Best Local Similarity 96.2%; Pred. No. 1.7e-20;
 Matches 50; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLWNPFI 52
 Db 624 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLWNPFI 675

RESULT 6

O90SM7 PRELIMINARY; PRT; 856 AA.
 AC O90SM7;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HXB2;
 RA Adamson-Onal Y., Cheynet V., Verrier B.;
 RT "Mutations and transcriptional alterations associated with the
 RT downregulation of HIV-1 envelope glycoprotein expression following
 RT acute cytopathic effects."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF358141; AAK49977.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 856 AA; 97126 MW; 9458D02B2FD734B3 CRC64;

Query Match 95.2%; Score 276; DB 15; Length 856;
 Best Local Similarity 94.2%; Pred. No. 2.5e-20;
 Matches 49; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLWNPFI 52
 Db 624 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLWNPFI 675

RESULT 7

O89797 PRELIMINARY; PRT; 852 AA.
 AC O89797;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM90-2;
 RX MEDLINE=95127297; PubMed=7826699.
 RA Reitz M., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.,
 RA Shaw G., Kong L., Weiss S., Waters D., Gallo R., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type IIIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LM90-2;
 RA Mulder K.E.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U12035; AAA76685.1; -;
 DR EMBL: U12036; AAA76671.1; -;
 DR InterPro: IPR000328; Env_Gp41.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 SQ SEQUENCE 852 AA; 96347 MW; 4E86522D4EB33CF CRC64;

Query Match 94.1%; Score 273; DB 15; Length 852;
 Best Local Similarity 94.2%; Pred. No. 5.1e-20;
 Matches 49; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLWNPFI 52
 Db 620 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLWNPFI 671

RESULT 8

O92877 PRELIMINARY; PRT; 856 AA.
 AC O92877;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=57667;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9908984; PubMed=9882298;
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B.A., Hofmann W.,
 RA Steenbeke T., Halloran M., Fanton J.W., Axthelm M.K., Letvin N.L.,
 RA Sodroski J.G.;
 RT "Changes in human immunodeficiency virus type 1 envelope glycoproteins
 RT responsible for the pathogenicity of a multiply passaged simian-human
 RT immunodeficiency virus (SHIV-HXB2)."
 RL J. Virol. 73:976-984(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cayabyab M., Karlsson G.B., Etamad-Moghadam B., Hofmann W.,
 RA Halloran M., Axthelm M.K., Letvin N.L., Sodroski J.G.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF041850; AAD12142.1; -;
 DR InterPro: IPR000328; Env_Gp41.

Query Match 94.1%; Score 273; DB 15; Length 852;
 Best Local Similarity 94.2%; Pred. No. 5.1e-20;
 Matches 49; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 856 AA; 97151 MW; C50BE0388FB73659 CRC64;

Query Match 93.1%; Score 270; DB 15; Length 856;
 Best Local Similarity 92.3%; Pred. No. 1e-19;
 Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLEESQNOEKLEQDELELDKWSLMMNFI 52
 DB 624 NHTTWLEMDREINNTSLHSLEESQNOEKLEQDELELDKWSLMMNFI 675

RESULT 9
 OY93A6 PRELIMINARY; PRT; 645 AA.
 AC 0993A6
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Truncated envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1007;
 RX MEDLINE=21192672; PubMed=11287644;
 RA Surman S., Lockett T.D., Siodod K.S., Jones B., Riberty J.M.,
 White S.W., Doherty P.C., Hurwitz J.L.;
 RT "Localization of CD4+ T cell epitope hotspots to exposed strands of
 RT HIV envelope glycoprotein suggests structural influences on antigen
 RT processing.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4587-4592(2001).
 DR EMBL: AF321563; AKI810.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KM Transmembrane.
 FT NON_TER
 SQ SEQUENCE 645 AA; 72485 MW; B076514BE93632EC CRC64;

Query Match 92.4%; Score 268; DB 15; Length 645;
 Best Local Similarity 92.3%; Pred. No. 1.2e-19;
 Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLEESQNOEKLEQDELELDKWSLMMNFI 52
 DB 593 NHTTWLEMDREINNTSLHSLEESQNOEKLEQDELELDKWSLMMNFI 644

RESULT 10
 OY82A3 PRELIMINARY; PRT; 851 AA.
 AC 0782A3
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Env polypeptide.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carolin F., Federic M., Equestre M., Ricci S., Ratti G., Zibai O.,
 RA Verani P., Rossi G.B.;
 RT "Sequence analysis of HIV-1 proviral DNA from a non producer

RT chronically infected HUT-78 cellular clone.";
 RL J. Viral Diseases 1:40-55(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352106; PubMed=2765297;
 RA Federico M., Tittl F., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Macchi B., Mangiano N., Verani P., Rossi G.;
 RT "Biological and molecular characterization of producer and non
 RT producer clones from HUT-78 infected with a patient HIV isolate.";
 RL AIDS Res. Hum. Retroviruses 5:385-396(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Tittl F., Federico M., Butto S., Orecchia A., Carlini F., Taddeo B.,
 RA Borsetti A., Saggio I., Verani P., Rossi G.;
 RT "Variability of HIV-1 virus: characteristics of an infected but not
 RT productive clone.";
 RL Int. J. Immunopharmacol. 3:17-23(1990).
 DR EMBL: Z11530; CAA77628.1; -;
 DR InterPro: IPR000328; Env_GP41.
 DR Pfam: PF00516; GP120; 1.
 DR Pfam: PF00517; GP41; 1.
 KW AIDS; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 851 AA; 96630 MW; 1A3767B9B7E98027 CRC64;

Query Match 92.4%; Score 268; DB 15; Length 851;
 Best Local Similarity 92.3%; Pred. No. 1.7e-19;
 Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTSLHSLEESQNOEKLEQDELELDKWSLMMNFI 52
 DB 619 NHTTWLEMDREINNTSLHSLEESQNOEKLEQDELELDKWSLMMNFI 670

RESULT 11
 OY85B2 PRELIMINARY; PRT; 854 AA.
 AC 085B2;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Envelope polypeptide.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86281827; PubMed=3016298;
 RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
 RA Martin M.A.;
 RT "Production of acquired immunodeficiency syndrome-associated
 RT retrovirus in human and nonhuman cells transfected with an infectious
 RT molecular clone.";
 RL J. Virol. 59:284-291(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Buckler C.E.;
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92219406; PubMed=1373204;
 RA Dai L.C., Littau R., Takahashi K., Ennis F.A.;
 RT "Mutation of human immunodeficiency virus type 1 at amino acid 585 on
 RT gp41 results in loss of killing by CD8+ A24-restricted cytotoxic T
 RT lymphocytes.";
 RL J. Virol. 66:3151-3154(1992).
 DR EMBL: M19921; AAA44992.1; -;
 DR InterPro: IPR000328; Env_GP41.

DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 854 AA; 97124 MW; ABA0A1BF36D55595A CRC64;
Query Match 92.4%; Score 268; DB 15; Length 854;
Best Local Similarity 92.3%; Pred. No. 1.7e-19;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 52
DB 622 NNTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 673
RESULT 12
OY 072502 PRELIMINARY; PRT; 854 AA.
AC 072502;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Env. Polyprotein.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE=96036482; PubMed=7483282;
RA Salminen M.O., Koch C., Sanders-Buell E., Ehrenberg P.K.,
RA Michael N.L., Carr J.K., Burke D.S., McCutchan F.E.;
RT "Recovery of virtually full-length HIV-1 provirus of diverse subtypes
from primary virus cultures using the polymerase chain reaction.";
RL Virology 213:80-86(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NL4-3;
RX MEDLINE=86281827; PubMed=3016298;
RA Adachi A., Gendelman H.E., Koenig S., Folks T., Willey R., Rabson A.,
RA Martin M.A.;
RT "Production of acquired immunodeficiency syndrome-associated
retrovirus in human and nonhuman cells transfected with an infectious
molecular clone.";
RL J. Virol. 59:284-291(1986).
DR EMBL: U26942; AAB60578.1; -;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
FT CONFLICT 214 H -> L (IN REF. 2).
FT CONFLICT 530 A -> S (IN REF. 2).
FT CONFLICT 739 739 G -> D (IN REF. 2).
SQ SEQUENCE 854 AA; 97005 MW; FF2264B3841D1220 CRC64;
Query Match 92.4%; Score 268; DB 15; Length 854;
Best Local Similarity 92.3%; Pred. No. 1.7e-19;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 52
DB 622 NNTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 673
RESULT 13
OY 074599 PRELIMINARY; PRT; 856 AA.
AC 074599;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE Env.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
(HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MCK1;
RA Iwataki Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86068; BAA12995.1; -;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 856 AA; 97287 MW; 238042A234C5685 CRC64;
Query Match 92.4%; Score 268; DB 15; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.7e-19;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 52
DB 624 NNTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 675
RESULT 14
OY 074090 PRELIMINARY; PRT; 856 AA.
AC 074090;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Env.
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RX MEDLINE=90101366; PubMed=1688473;
RA Cloyd M.W., Moore B.E.;
RT "Spectrum of Biological Properties of Human Immunodeficiency Virus
(HIV-1) Isolates.";
RL Virology 174:103-116(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PM213;
RA Iwataki Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86069; BAA13003.1; -;
DR InterPro: IPR000328; Env.GP41.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS: Coat protein; Glycoprotein; Polypeptide; Transmembrane.
SQ SEQUENCE 856 AA; 97396 MW; FE3E784C423C108C CRC64;
Query Match 92.4%; Score 268; DB 15; Length 856;
Best Local Similarity 92.3%; Pred. No. 1.7e-19;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKWSLWNPNI 52

Db 624 NNMTMWEWDREINNNTSLHSLIEESONOEKNEQELLEDKWSLMMNPMI 675

RESULT 15

090178 PRELIMINARY; PRT; 854 AA.
 AC 090178;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE Envelope glycoprotein.
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxId=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95074930; PubMed=7983770;
 RA Fang H., Pincus S.H.;
 RT "Unique insertion sequence and pattern of CD4 expression in variants
 RT selected with immunotoxins from human immunodeficiency virus type 1-
 RT infected T cells.";
 RL J. Virol. 69:75-81(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Fang H., Pincus S.H.;
 RT "Spontaneous activation of human immunodeficiency virus type 1 in an
 RT immunotoxin-resistant variant T cell line.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF070521; AAC28452.1; -
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW Aids; Coat protein; Glycoprotein; Polypeptide; Transmembrane.
 SQ SEQUENCE 854 AA; 96885 MW; 0808F3AED27C693B CRC64;

Query Match 91.0%; Score 264; DB 15; Length 854;
 Best Local Similarity 90.4%; Pred. No. 4.3e-19;
 Matches 47; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNNTSLHSLIEESONOEKNEQELLEDKWSLMMNPMI 52
 I:|||||
 Db 622 NNMTMWEWDREINNNTSLHSLIEESONOEKNEQELLEDKWSLMMNPMI 673

Search completed: May 7, 2003, 09:57:23
 Job time : 38.3148 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:51:07 ; Search time 15.4074 Seconds

(without alignments)
99,302 Million cell updates/sec

Title: US-09-877-606-9

Perfect score: 290
Sequence: 1 NHTTWLEMDREINNTSLIH.....LQELLELDKASLNNWENI 52Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :

- 1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/1/aa/PCFUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/aa/ackfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	281	96.9	138	4	US-09-570-921-20
2	281	96.9	138	4	US-09-570-921-21
3	281	96.9	268	4	US-08-965-056-16
4	281	96.9	345	4	US-09-272-342B-7
5	281	96.9	519	1	US-08-589-446-8
6	281	96.9	519	1	US-08-444-882-8
7	281	96.9	519	2	US-08-389-459A-8
8	281	96.9	519	3	US-08-987-867A-8
9	281	96.9	856	2	US-07-916-098A-2
10	281	96.9	856	4	US-09-337-387-11
11	281	96.9	138	4	US-09-570-921-22
12	281	96.9	138	4	US-09-570-921-24
13	281	96.9	138	4	US-09-570-921-26
14	281	96.9	138	4	US-09-570-921-58
15	281	96.9	237	3	US-08-388-353-641
16	281	96.9	237	3	US-08-488-551B-641
17	281	96.9	268	4	US-08-965-056-17
18	281	96.9	268	4	US-08-965-056-18
19	281	96.9	268	5	PCR-US95-13335-1
20	281	96.9	338	3	US-08-486-099-90
21	281	96.9	338	3	US-08-360-107A-100
22	281	96.9	338	3	US-08-484-223B-90
23	281	96.9	338	3	US-08-919-597-90
24	281	96.9	338	3	US-08-475-668A-90
25	281	96.9	338	3	US-08-485-551A-90
26	281	96.9	338	3	US-08-471-913A-90
27	281	96.9	338	4	US-08-485-264A-90

28	268	92.4	338	4	US-08-474-349A-90	Sequence 90, Appl
29	268	92.4	338	4	US-08-255-208A-26	Sequence 26, Appl
30	268	92.4	345	4	US-08-817-441-49	Sequence 49, Appl
31	268	92.4	615	4	US-09-257-490-11	Sequence 11, Appl
32	268	92.4	826	1	US-08-375-510-2	Sequence 2, Appl
33	268	92.4	826	2	US-08-487-657-2	Sequence 2, Appl
34	268	92.4	839	4	US-08-472-240A-10	Sequence 10, Appl
35	268	92.4	834	4	US-09-309-572-23	Sequence 23, Appl
36	268	92.4	856	4	US-09-124-900-9	Sequence 9, Appl
37	268	92.4	861	1	US-08-127-499A-14	Sequence 14, Appl
38	268	92.4	861	1	US-08-482-847-14	Sequence 14, Appl
39	268	92.4	861	4	US-07-956-483-10	Sequence 10, Appl
40	268	92.4	861	4	US-07-956-483-16	Sequence 16, Appl
41	268	92.4	861	4	US-08-472-240A-1	Sequence 1, Appl
42	268	92.4	861	4	US-08-472-240A-7	Sequence 7, Appl
43	268	92.4	861	4	US-08-817-441-103	Sequence 103, App
44	268	92.4	863	3	US-08-463-210-11	Sequence 11, Appl
45	268	92.4	880	2	US-08-788-815-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-09-570-921-20
Sequence 20, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-20
Query Match 96.9%; Score 281; DB 4; Length 138;
Best Local Similarity 96.2%; Pred. No. 5e-24;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 NHTTWLEMDREINNTSLIHSLIEESONQOEKLEQELLELDKASLNNWENI 52
Db 85 NHTTWLEMDREINNTSLIHSLIEESONQOEKLEQELLELDKASLNNWENI 136
RESULT 2
US-09-570-921-21
Sequence 21, Application US/09570921
Patent No. 6455265
GENERAL INFORMATION:
APPLICANT: SERRES, PIERRE-FRANCOIS
TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
FILE REFERENCE: 106213
CURRENT APPLICATION NUMBER: US/09/570,921
CURRENT FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: PCT/FR98/02447
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: FR/97/14387
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 21
```

LENGTH: 138
TYPE: PRT
ORGANISM: Human
US-09-570-921-21

Query Match
Best Local Similarity 96.9%; Score 281; DB 4; Length 138;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLHSLIESQNOOEKLEQELLEDKRWASIMWNI 52
DB 85 NHTTWLEMDREINNTYSLHSLIESQNOOEKLEQELLEDKRWASIMWNI 136

RESULT 3
US-08-965-056-16
Sequence 16, Application US/08965056
Patent No. 6271198
GENERAL INFORMATION:

APPLICANT: Andrew C. Braisted
APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovashnik
APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-965-056-16

Query Match
Best Local Similarity 96.9%; Score 281; DB 4; Length 268;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLHSLIESQNOOEKLEQELLEDKRWASIMWNI 52
DB 154 NHTTWLEMDREINNTYSLHSLIESQNOOEKLEQELLEDKRWASIMWNI 205

RESULT 4
US-09-272-342B-7
Sequence 7, Application US/09272342B
Patent No. 6294341
GENERAL INFORMATION:
APPLICANT: YU, YEON-GYU

APPLICANT: KIM, SUNG-HOU
APPLICANT: RYU, JAE-RYEON
TITLE OF INVENTION: METHOD FOR DETECTING A SUBSTANCE HAVING AN ACTIVITY TO
TITLE OF INVENTION: INHIBIT HIV INFECTION USING IMMUNOSSAY AND VARIANT
TITLE OF INVENTION: PROTEIN USED FOR SAID METHOD
FILE REFERENCE: 2901-0125-0
CURRENT APPLICATION NUMBER: US/09/272,342B
CURRENT FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 345
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-09-272-342B-7

Query Match
Best Local Similarity 96.9%; Score 281; DB 4; Length 345;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNTYSLHSLIESQNOOEKLEQELLEDKRWASIMWNI 52
DB 113 NHTTWLEMDREINNTYSLHSLIESQNOOEKLEQELLEDKRWASIMWNI 164

RESULT 5
US-08-589-446-8
Sequence 8, Application US/08589446
Patent No. 5614413
GENERAL INFORMATION:

APPLICANT: Morrow, Casey D.
TITLE OF INVENTION: ENCAPSULATED POLIOVIRUS NUCLEIC
TITLE OF INVENTION: ACID AND METHODS OF MAKING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 STATE STREET, SUITE 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/589,446
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/087,009
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Geary III, William C.
REGISTRATION NUMBER: 31,359
REFERENCE/DOCKET NUMBER: UAG-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-589-446-8

Query Match
Best Local Similarity 96.9%; Score 281; DB 1; Length 519;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNYTSLHSLIEESONQOEKLEQELLELDKNASLMMWNI 52
DB 420 NHTTWLMDREINNYTSLHSLIEESONQOEKLEQELLELDKNASLMMWNI 471

RESULT 6
US-08-444-882-8
Sequence 8, Application US/08444882
Patent No. 5622705

GENERAL INFORMATION:

APPLICANT: MORROW, Casey D.

TITLE OF INVENTION: ENCAPSIDATED POLIOVIRUS NUCLEIC

TITLE OF INVENTION: ACID AND METHODS OF MAKING AND

TITLE OF INVENTION: USING SAME

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/444,882

FILING DATE: 19-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/087,009

FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Geary III, William C.

REGISTRATION NUMBER: 31,359

REFERENCE/DOCKET NUMBER: UAG-004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ. ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 519 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-444-882-8

Query Match 96.9%; Score 281; DB 1; Length 519;
Best Local Similarity 96.2%; Pred. No. 2,2e-23;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNYTSLHSLIEESONQOEKLEQELLELDKNASLMMWNI 52
DB 420 NHTTWLMDREINNYTSLHSLIEESONQOEKLEQELLELDKNASLMMWNI 471

RESULT 7
US-08-389-459A-8

Sequence 8, Application US/08389459A

Patent No. 5817512

GENERAL INFORMATION:

APPLICANT: MORROW, Casey D. and Porter, Donna, C.

TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS

TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND

TITLE OF INVENTION: USING SAME

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 STATE STREET, SUITE 510

CITY: BOSTON

STATE: MASSACHUSETTS

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/987,867A

FILING DATE: 09-DEC-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/087,009

FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: UAG-004CPDV

TELECOMMUNICATION INFORMATION:

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/389,459A

FILING DATE: 15-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/087,009

FILING DATE: 01-JUL-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Silverl, Jean M.

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: UAG-004CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ. ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 519 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-389-459A-8

Query Match 96.9%; Score 281; DB 2; Length 519;
Best Local Similarity 96.2%; Pred. No. 2,2e-23;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNYTSLHSLIEESONQOEKLEQELLELDKNASLMMWNI 52
DB 420 NHTTWLMDREINNYTSLHSLIEESONQOEKLEQELLELDKNASLMMWNI 471

RESULT 8
US-08-987-867A-8

Sequence 8, Application US/08987867A

Patent No. 6063384

GENERAL INFORMATION:

APPLICANT: C. Morrow et al.

TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL

TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND

TITLE OF INVENTION: USING SAME

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 STATE STREET

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/987,867A

FILING DATE: 09-DEC-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/087,009

FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Myers, Louis

REGISTRATION NUMBER: 35,965

REFERENCE/DOCKET NUMBER: UAG-004CPDV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-867A-8

Query Match	96.9%;	Score 281;	DB 3;	Length 519;
Best Local Similarity	96.2%;	Pred. No. 2.2e-23;		
Matches 50;	Conservative	1;	Mismatches	1;
				Indels

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OY      1 NHTTWLEMDREINNYTSLIHSLIEESQNOQEKLELLELDKWA$IMWNFNI 52
         ||||:|||||
Db      420 NHTTWMEWDREINNYTSLIHSLIEESQNOQEKNEQELLELDKWA$IMWNFNI 471

```

RESULT 9
US-07-916-098A-2

GENERAL INFORMATION:
APPLICANT: BURKLY, LINDA C.
APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WINCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE

Query Match	96.98;	Score 281;	DB 2;	Length 856;
Best Local Similarity	96.28;	Pred. No. 3.9e-23;		

Matches	50,	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
Oy	1	NHTTWLEWDREINNTSLIHS	LI	EESSNQOEKLEQELLELDK	WASIMNNFNI	52			
		:							
Db	624	NHTTWLEWDREINNTSLIHS	LI	EESSNQOEKLEQELLELDK	WASIMNNFNI	675			

RESULT 10
US-09-337-387-11
; Sequence 11, Application US/09337387
; Patent No. 6420545

```

: GENERAL INFORMATION:
: APPLICANT: HOXIE, James A.
: APPLICANT: LABRANCHE, Celia C.
: APPLICANT: DOMS, Robert W.
: APPLICANT: HOFEMAN, Trevor L.
: TITLE OF INVENTION: CD4-INDEPENDENT HIV ENVELOPE PROTEINS AS VACCINES AND
: TITLE OF INVENTION: THERAPEUTICS
: FILE REFERENCE: Hoxie 9596-10/01 (0282)
: CURRENT APPLICATION NUMBER: US/09/337,387
: CURRENT FILING DATE: 1999-06-22
: PRIOR APPLICATION NUMBER: US 09/317,556
: PRIOR FILING DATE: 1999-05-24
: NUMBER OF SEQ ID NOS: 12
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 11
: LENGTH: 856
: TYPE: PRT
: ORGANISM: Human Immunodeficiency virus type 1
: US-09-337-387-11

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Query Match	96.98;	Score 281;	DB 4;	Length 856;
Best Local Similarity	96.28;	Pred. No. 3.9e-23;		
Matches 50; Conservative	1;	Mismatches 1;	Indels 0;	Gaps 0;

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QY 1 NHTTWLEWMDREINNTSLIHSLSIESQNOQEKLEQELLELDKASLMMWFI 52
      ||||:||||||||||||||||||||||||||||||||||||||||||
Db 624 NHTTWNEWMDREINNTSLIHSLSIESQNOQEKNEQELLELDKASLMMWFI 675
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RESULT 11
 US-09-570-921-22
 : Sequence 22, Application US/09570921
 : Patent No. 6455265
 : GENERAL INFORMATION:
 : APPLICANT: SERRES, PIERRE-FRANCOIS
 : TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
 : TITLE OF INVENTION: PATHOGENIC EFFECTS RELATED TO A RETROVIRAL INFECTION
 : FILE REFERENCE: 106213
 : CURRENT APPLICATION NUMBER: US/09/570,921
 : CURRENT FILING DATE: 2000-05-15
 : PRIOR APPLICATION NUMBER: PCT/FR98/02447
 : PRIOR FILING DATE: 1998-11-17
 : PRIOR APPLICATION NUMBER: FR/97/14387
 : PRIOR FILING DATE: 1997-11-17
 : NUMBER OF SEQ ID NOS: 144
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 22
 : LENGTH: 138
 : TYPE: PRF
 : ORGANISM: Human
 : US-09-570-921-22

Query Match	92.48;	Score 268;	DB 4;	Length 138;
Best Local Similarity	92.38;	Pred. No. 1.3e-22;		
Matches 48;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;

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Qy      1 NHTTLEWMDREINNTYSLIHSLIEESQNQQEKLQEELLELDKWSLWNFNI    52  
       | : ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db     85 NNHMTWMEMDREINNTYSLIHSLIEESQNQQEKNEDELLDKWSLWNFNI   136
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RESULT 12

US-09-570-921-24
; Sequence 24, Application US/09570921
; Patent No. 6455265
; GENERAL INFORMATION:
; APPLICANT: SERRES, PIERRE-FRANCOIS
; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
; FILE REFERENCE: 106213
; CURRENT APPLICATION NUMBER: US/09/570,921
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: PCT/FR98/02447
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: FR/97/14387
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
US-09-570-921-24

Query Match 92.4%; Score 268; DB 4; Length 138;
Best Local Similarity 92.3%; Pred. No. 1.3e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTWTLEMDREINNTYSLIHSIESONQOEKLELDKASLNNWFI 52
Db 85 NMTWMEWDREINNTYSLIHSIESONQOEKNEQLELDKASLNNWFI 136

RESULT 13
US-09-570-921-26
; Sequence 26, Application US/09570921
; Patent No. 6455265
; GENERAL INFORMATION:
; APPLICANT: SERRES, PIERRE-FRANCOIS
; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
; FILE REFERENCE: 106213
; CURRENT APPLICATION NUMBER: US/09/570,921
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: PCT/FR98/02447
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: FR/97/14387
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
US-09-570-921-26

Query Match 92.4%; Score 268; DB 4; Length 138;
Best Local Similarity 92.3%; Pred. No. 1.3e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTWTLEMDREINNTYSLIHSIESONQOEKLELDKASLNNWFI 52
Db 85 NMTWMEWDREINNTYSLIHSIESONQOEKNEQLELDKASLNNWFI 136

RESULT 14
US-09-570-921-58
; Sequence 58, Application US/09570921
; Patent No. 6455265
; GENERAL INFORMATION:
; APPLICANT: SERRES, PIERRE-FRANCOIS
; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
; FILE REFERENCE: 106213
; CURRENT APPLICATION NUMBER: US/09/570,921

CURRENT FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: PCT/FR98/02447
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: FR/97/14387
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 58
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
US-09-570-921-58

Query Match 92.4%; Score 268; DB 4; Length 138;
Best Local Similarity 92.3%; Pred. No. 1.3e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTWTLEMDREINNTYSLIHSIESONQOEKLELDKASLNNWFI 52
Db 85 NMTWMEWDREINNTYSLIHSIESONQOEKNEQLELDKASLNNWFI 136

RESULT 15
US-08-388-353-641
; Sequence 641, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Leamont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 641:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 237 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-388-353-641

Query Match 92.4%; Score 268; DB 3; Length 237;
Best Local Similarity 92.3%; Pred. No. 2.5e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTWTLEMDREINNTYSLIHSIESONQOEKLELDKASLNNWFI 52

Wed May 7 14:34:41 2003

us-09-877-606-9.ra1

Page 6

Db 5 NNPTMMDREINNYTSLHSLIBESONQOEKNEOELELDKRNASLWPFNI 56

Search completed: May 7, 2003, 09:59:52
Job time : 15.4074 secs

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OM protein - protein search, using sw model

Run on: May 7, 2003, 09:57:27 ; Search time 28.6481 Seconds

(without alignments)
167,038 Million cell updates/sec

Title: US-09-877-606-9

Perfect score: 290
Sequence: 1 NHTTWLEMDREINNTYSLIH.....LQELLELDKMSLNMENI 52

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	281	96.9	268	10	US-09-854-816-16
2	281	96.9	344	9	US-10-040-349B-1
3	281	96.9	519	10	US-09-756-551A-8
4	281	96.9	856	10	US-09-476-242-1
5	268	92.4	56	10	US-09-779-451-4
6	268	92.4	177	9	US-10-040-349B-2
7	268	92.4	221	9	US-10-059-271-84
8	268	92.4	232	9	US-10-059-271-81
9	268	92.4	254	9	US-10-059-271-82
10	268	92.4	256	9	US-10-059-271-97
11	268	92.4	268	10	US-09-854-816-17
12	268	92.4	268	10	US-09-854-816-18
13	268	92.4	345	9	US-10-026-741-48
14	268	92.4	345	10	US-09-779-451-8
15	268	92.4	391	9	US-10-059-271-93
16	268	92.4	853	9	US-10-003-035-33
17	268	92.4	861	9	US-10-026-741-103
18	268	92.4	1101	9	US-10-003-035-53
19	268	92.4	1186	9	US-10-003-035-53

20	265	91.4	268	10	US-09-854-816-19	Sequence 19, Appl
21	251	86.6	269	10	US-09-854-816-46	Sequence 46, Appl
22	250	86.2	268	10	US-09-854-816-13	Sequence 13, Appl
23	247	85.2	46	10	US-09-779-451-41	Sequence 41, Appl
24	246	84.8	269	10	US-09-854-816-43	Sequence 43, Appl
25	245	84.5	268	10	US-09-854-816-9	Sequence 9, Appl
26	244	84.1	269	10	US-09-854-816-12	Sequence 12, Appl
27	243	83.8	269	10	US-09-854-816-28	Sequence 28, Appl
28	242	83.4	268	10	US-09-854-816-26	Sequence 26, Appl
29	242	83.4	619	10	US-09-891-609-4	Sequence 4, Appl
30	242	83.4	646	10	US-09-891-609-2	Sequence 2, Appl
31	242	83.4	847	10	US-09-476-242-2	Sequence 47, Appl
32	241	83.1	233	10	US-09-854-816-50	Sequence 50, Appl
33	239	82.4	269	10	US-09-854-816-44	Sequence 44, Appl
34	238	82.1	268	10	US-09-854-816-8	Sequence 8, Appl
35	238	82.1	579	9	US-10-032-162-15	Sequence 15, Appl
36	238	82.1	625	9	US-10-032-162-17	Sequence 17, Appl
37	238	82.1	643	9	US-10-032-162-13	Sequence 13, Appl
38	237	81.7	268	10	US-09-854-816-41	Sequence 41, Appl
39	234	80.7	267	10	US-09-854-816-38	Sequence 38, Appl
40	234	80.7	269	10	US-09-854-816-32	Sequence 32, Appl
41	234	80.7	269	10	US-09-854-816-34	Sequence 34, Appl
42	234	80.7	269	10	US-09-854-816-45	Sequence 45, Appl
43	233	80.3	267	10	US-09-854-816-15	Sequence 15, Appl
44	233	80.3	269	10	US-09-854-816-6	Sequence 6, Appl
45	232	80.0	267	10	US-09-854-816-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-09-854-816-16
Sequence 16, Application US/09854816
Patent No. US20020151473A1
GENERAL INFORMATION:
APPLICANT: Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovaanik
James A. Wells
TITLE OF INVENTION: Constrained Helical Peptides and Methods of Making Same
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854, 816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965, 056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:

LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-854-816-16

Query Match 96.9%; Score 281; DB 10; Length 268;
Best Local Similarity 96.2%; Pred. No. 2,4e-23;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNTYSLHSLIESQNOQEKLEDELLDLKWSLMMNFI 52
DB 154 NHTTWMDREINNTYSLHSLIESQNOQEKNEDELLDLKWSLMMNFI 205

RESULT 2
US-10-040-349B-1

Sequence 1, Application US/10040349B
Publication No. US20030082521A1
GENERAL INFORMATION:
APPLICANT: Brasseur, Robert
APPLICANT: Charleaux, Benoit
APPLICANT: Chevalier, Michel
APPLICANT: El Hadid, Raphaelle
APPLICANT: Krell, Tino
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
FILE REFERENCE: 01-078-A
CURRENT APPLICATION NUMBER: US/10/040,349B
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 344
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
NAME/KEY: Peptide
LOCATION: (1)..(344)
OTHER INFORMATION: gp41 IAI protein
US-10-040-349B-1

Query Match 96.9%; Score 281; DB 9; Length 344;
Best Local Similarity 96.2%; Pred. No. 3,1e-23;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNTYSLHSLIESQNOQEKLEDELLDLKWSLMMNFI 52
DB 113 NHTTWMDREINNTYSLHSLIESQNOQEKNEDELLDLKWSLMMNFI 164

RESULT 3
US-09-756-551A-8

Sequence 8, Application US/09756551A
Patent No. US20020051768A1
GENERAL INFORMATION:
APPLICANT: C. Morrow et al.
TITLE OF INVENTION: ENCAPSULATED RECOMBINANT VIRAL
TITLE OF INVENTION: NUCLEIC ACID AND METHODS OF MAKING AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/756,551A
FILING DATE: 08-JAN-2001
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/376,184
FILING DATE: 17-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,867
FILING DATE: 09-DEC-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/389,459
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,009
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lauro, Peter C.
REGISTRATION NUMBER: 32,360
REFERENCE/DOCKET NUMBER: UAI-004CPDVZCN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-756-551A-8

Query Match 96.9%; Score 281; DB 10; Length 519;
Best Local Similarity 96.2%; Pred. No. 4,9e-23;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNTYSLHSLIESQNOQEKLEDELLDLKWSLMMNFI 52
DB 420 NHTTWMDREINNTYSLHSLIESQNOQEKNEDELLDLKWSLMMNFI 471

RESULT 4
US-09-476-242-1

Sequence 1, Application US/09476242
Patent No. US2002014683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: BARROG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605,002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 856
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-476-242-1

Query Match 96.9%; Score 281; DB 10; Length 856;
Best Local Similarity 96.2%; Pred. No. 8,4e-23;
Matches 50; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NHTTWLMDREINNTYSLHSLIESQNOQEKLEDELLDLKWSLMMNFI 52
DB 624 NHTTWMDREINNTYSLHSLIESQNOQEKNEDELLDLKWSLMMNFI 675

RESULT 5
US-09-779-451-4
Sequence 4, Application US/09779451

Patent No. US20020094521A1
GENERAL INFORMATION:
APPLICANT: Wild, Carl T.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 56
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-4

Query Match 92.4%; Score 268; DB 10; Length 56;
Best Local Similarity 92.3%; Pred. No. 1,1e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLIHSLEESONQOEKLEQELLELDKWSLNNWFI 52
|:|:|||||
DB 2 NNTWMEDEINNYTSLIHSLEESONQOEKNEQELLELDKWSLNNWFI 53

RESULT 6
US-10-040-349B-2
Sequence 2, Application US/10040349B
Publication No. US20030082521A1
GENERAL INFORMATION:
APPLICANT: Brasseur, Robert
APPLICANT: Charleaux, Benoit
APPLICANT: Chevalier, Michel
APPLICANT: El Habib, Raphaelle
APPLICANT: Krell, Tino
TITLE OF INVENTION: Polypeptide Inducing Antibodies Neutralizing HIV
FILE REFERENCE: 01-078-7
CURRENT APPLICATION NUMBER: US/10/040,349B
CURRENT FILING DATE: 2002-07-09
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 177
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
NAME/KEY: Peptide
LOCATION: (1)..(177)
OTHER INFORMATION: polypeptide derived from gp41 LAI
US-10-040-349B-2

Query Match 92.4%; Score 268; DB 9; Length 177;
Best Local Similarity 92.3%; Pred. No. 4e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLIHSLEESONQOEKLEQELLELDKWSLNNWFI 52
|:|:|||||
DB 90 NNTWMEDEINNYTSLIHSLEESONQOEKNEQELLELDKWSLNNWFI 141

RESULT 7
US-10-059-271-84
Sequence 84, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPKE, HEINRICH
APPLICANT: BUDD, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND

TITLE OF INVENTION: BEING IMMOBILIZED
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
LENGTH: 221
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-84

Query Match 92.4%; Score 268; DB 9; Length 221;
Best Local Similarity 92.3%; Pred. No. 5e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLIHSLEESONQOEKLEQELLELDKWSLNNWFI 52
|:|:|||||
DB 117 NNTWMEDEINNYTSLIHSLEESONQOEKNEQELLELDKWSLNNWFI 168

RESULT 8
US-10-059-271-81
Sequence 81, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPKE, HEINRICH
APPLICANT: BUDD, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 232
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-81

Query Match 92.4%; Score 268; DB 9; Length 232;
Best Local Similarity 92.3%; Pred. No. 5.3e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHTTWLEMDREINNYTSLIHSLEESONQOEKLEQELLELDKWSLNNWFI 52
|:|:|||||
DB 130 NNTWMEDEINNYTSLIHSLEESONQOEKNEQELLELDKWSLNNWFI 181

RESULT 9
US-10-059-271-82
Sequence 82, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPKE, HEINRICH
APPLICANT: BUDD, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271

;; CURRENT FILING DATE: 2002-01-31
;; PRIOR APPLICATION NUMBER: DE 101 06 295
;; PRIOR FILING DATE: 2001-02-02
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 82
;; LENGTH: 254
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; US-10-059-271-82

Query Match 92.4%; Score 268; DB 9; Length 254;
Best Local Similarity 92.3%; Pred. No. 5.9e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTYSLIHSILIESQNOQEKLELLELDKWSIWMNFNI 52
|:|||||||||||||||||||||||||||||||||||||||||

Db 152 NNMTWMEWDREINNTYSLIHSILIESQNOQEKNEQLELDKWSIWMNFNI 203

RESULT 10
US-10-059-271-97
; Sequence 97, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
; APPLICANT: REPERE, HEINRICH
; APPLICANT: BUDE, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 97
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
; US-10-059-271-97

Query Match 92.4%; Score 268; DB 9; Length 256;
Best Local Similarity 92.3%; Pred. No. 5.9e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTYSLIHSILIESQNOQEKLELLELDKWSIWMNFNI 52
|:|||||||||||||||||||||||||||||||||||||||||

Db 152 NNMTWMEWDREINNTYSLIHSILIESQNOQEKNEQLELDKWSIWMNFNI 203

RESULT 11
US-09-854-816-17
; Sequence 17, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; MAKING SAME
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-854-816-17

Query Match 92.4%; Score 268; DB 10; Length 268;
Best Local Similarity 92.3%; Pred. No. 6.2e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNTYSLIHSILIESQNOQEKLELLELDKWSIWMNFNI 52
|:|||||||||||||||||||||||||||||||||||||||||

Db 154 NNMTWMEWDREINNTYSLIHSILIESQNOQEKNEQLELDKWSIWMNFNI 205

RESULT 12
US-09-854-816-18
; Sequence 18, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovasnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; MAKING SAME
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/854,816
FILING DATE: 15-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/965,056
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-854-816-18

Query Match 92.4%; Score 268; DB 10; Length 268;
Best Local Similarity 92.3%; Pred. No. 6.2e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLMMWNI 52
|:|:|||||||||||||||||||||||||||||||||||||||||
Db 154 NNMTWEMDREINNYTSLHSLIEESONQOEKNEQELLELDKASLMMWNI 205

RESULT 13
US-10-026-741-49
Sequence 49, Application US/10026741
Publication No. US20030049604A1
GENERAL INFORMATION:
APPLICANT: CHARNEAU, PIERRE
CLAVEY, FRANCOISE
BORMAN, ANDRE
OUILLET, CAROLINE
GUERARD, DENISE
MONTAGNIER, LUC
DOMJON DE SAINT-MARTIN, JACQUELINE
COHEN, JACQUES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
SUBTYPE) ANTIGENS
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunnet, L.L.P.
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/026,741
FILING DATE: 27-Dec-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/817,441
FILING DATE: 31-Aug-1998
APPLICATION NUMBER: PCT/FR 95/01391
FILING DATE: 20-OCT-1995
APPLICATION NUMBER: FR 9412554
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: FR 9502526
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000

TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-026-741-49

Query Match 92.4%; Score 268; DB 9; Length 345;
Best Local Similarity 92.3%; Pred. No. 8.2e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLMMWNI 52
|:|:|||||||||||||||||||||||||||||||||||||||||
Db 113 NNMTWEMDREINNYTSLHSLIEESONQOEKNEQELLELDKASLMMWNI 164

RESULT 14
US-09-779-451-8
Sequence 8, Application US/09779451
Patent No. US20020094521A1
GENERAL INFORMATION:
APPLICANT: Allaway, Carl T.
TITLE OF INVENTION: Assay for Detection of Viral Fusion Inhibitors
FILE REFERENCE: 1900.0300003
CURRENT APPLICATION NUMBER: US/09/779,451
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/235,901
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/181,543
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 77
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 345
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-8

Query Match 92.4%; Score 268; DB 10; Length 345;
Best Local Similarity 92.3%; Pred. No. 8.2e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 NHTTWLEMDREINNYTSLHSLIEESONQOEKLEQELLELDKASLMMWNI 52
|:|:|||||||||||||||||||||||||||||||||||||||||
Db 113 NNMTWEMDREINNYTSLHSLIEESONQOEKNEQELLELDKASLMMWNI 164

RESULT 15
US-10-059-271-93
Sequence 93, Application US/10059271
Publication No. US20030082208A1
GENERAL INFORMATION:
APPLICANT: REPKKE, HEINRICH
APPLICANT: BUDDER, ECKHARD
APPLICANT: NICOLAUS, STEFAN
TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
FILE REFERENCE: ALBRE-22
CURRENT APPLICATION NUMBER: US/10/059,271
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: DE 101 06 295
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
LENGTH: 391
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-059-271-93

Query Match 92.4%; Score 268; DB 9; Length 391;
Best Local Similarity 92.3%; Pred. No. 9, 4e-22;
Matches 48; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 NHPTWLEMDREINNTYSLIHSLIESQNOQEKLEQELLEDKWSLNNFNI 52
|:|:|||||||||||||||||||||||||||||||||||||
Db 155 NNMTWMEHMDREINNTYSLIHSLIESQNOQEKLEQELLEDKWSLNNFNI 206

Search completed: May 7, 2003, 10:21:56
Job time : 29.6481 secs